

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 16, 2003, 08:03:44 : Search time 259.494 Seconds
(without alignments)
9364.023 Million cell updates/sec

Title: US-09-710-058a-1
Perfect score: 1079
Sequence: 1 ggtatatacaacagtgatcgc.....gtataaaaaaaaaaaaaaaaa 1079

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 1125959159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: N.Geneseq_101002.*
2: /SID52/gcqdtaa/geneseq/geneseqn-emb1/NA1980.DAT.*
3: /SID52/gcqdtaa/geneseq/geneseqn-emb1/NA1981.DAT.*
4: /SID52/gcqdtaa/geneseq/geneseqn-emb1/NA1982.DAT.*
5: /SID52/gcqdtaa/geneseq/geneseqn-emb1/NA1983.DAT.*
6: /SID52/gcqdtaa/geneseq/geneseqn-emb1/NA1984.DAT.*
7: /SID52/gcqdtaa/geneseq/geneseqn-emb1/NA1985.DAT.*
8: /SID52/gcqdtaa/geneseq/geneseqn-emb1/NA1986.DAT.*
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11: /SID52/gcqdtaa/geneseq/geneseqn-emb1/NA1989.DAT.*
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21: /SID52/gcqdtaa/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SID52/gcqdtaa/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SID52/gcqdtaa/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SID52/gcqdtaa/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1077.4	59.9	1079	20	AAZ27547
2	1077.4	99.9	1079	22	AAAF89808
3	1077.4	99.9	1079	24	AAAD22198
4	534.4	49.5	720	22	AAAF46937
5	534.4	49.5	720	24	AAAF3693
6	392.6	36.4	1104	20	AAZ27548
7	392.6	36.4	1104	22	AAAF89809
8	392.6	36.4	1104	24	AAZ22207
9	391.6	36.3	1279	20	AAZ27549

10	391.6	36.3	1279	22	AAAF89810
11	391.6	36.3	1279	24	AAZ22208
12	336	31.1	720	22	AAAF46938
13	336	31.1	720	24	AAAF3694
14	237.8	22.0	860	24	AAZ22203
15	229	21.2	860	24	AAZ22204
16	227.4	21.1	864	24	AAZ22202
17	199.2	18.5	780	22	AAAF380
18	165.2	15.3	864	24	AAZ22205
19	161.4	15.0	801	22	AAZ22206
20	161.4	15.0	801	22	AAZ22207
21	161.4	15.0	801	22	AAZ22208
22	161	14.9	1116	21	AAAF2766
23	161	14.9	1116	22	AAZ03611
24	150.6	14.0	850	22	AAZ03614
25	145.6	13.5	962	24	AAAF6991
26	138.6	12.8	699	22	AAZ13052
27	138.6	12.8	699	22	AAZ11141
28	138.6	12.8	699	22	AAZ47653
29	138.6	12.8	960	21	AAZ28862
30	134.8	12.5	666	24	AAZ61142
31	134.8	12.5	678	22	AAZ13053
32	134.8	12.5	678	22	AAZ11142
33	134.8	12.5	678	22	AAZ47654
34	134.8	12.5	678	24	AAZ95921
35	134.8	12.5	859	24	AAZ47952
36	132.6	12.3	908	24	AAZ41168
37	131	12.1	910	24	AAZ41167
38	131	12.1	910	24	AAZ41182
39	130.4	12.1	876	21	AAZ28958
40	130.4	12.1	876	22	AAZ03618
41	130.2	12.1	678	24	AAZ95922
42	129.4	12.0	681	24	AAZ41170
43	129.4	12.0	684	24	AAZ41169
44	129.4	12.0	684	24	AAZ41180
45	127.8	11.8	681	24	AAZ41171

ALIGNMENTS

RESULT 1	AAZ27547	AAZ27547 standard: DNA: 1079 BP.
AC	AAZ27547:	
XX		
DT	13-DEC-1999 (first entry)	
XX		
DE	Renilla mulleri green fluorescent protein coding sequence.	
KW	Luciferase: green fluorescent protein; GFP; screening assay; diagnosis;	
KW	bioluminescence-generating system; toy; cosmetic; fairy dust; beverage;	
KW	body paint; squirt gun; balloon; slimy play material; soap; toothpaste;	
KW	ds.	
XX		
OS	Renilla mulleri.	
XX		
PN	WO9949015-A2.	
XX		
PD	30-SEP-1999.	
XX		
PF	26-MAR-1999: 99WO-US06698.	
XX		
PR	27-MAR-1998: 98US-0079624.	
PR	15-JUN-1998: 98US-0089367.	
PR	01-OCT-1998: 98US-0102939.	
XX		
PA	(PROL-) PROLIME LTD.	
PA	(BRYA/) BRYAN B J.	
XX		
PI	Bryan BJ, Szent-Gyorgyi C;	
XX		

Nucleotide sequenc
Ptilosarcus gurney
R. reniformis huma
Humanised Renilla
Renilla reniformis
Renilla reniformis
Renilla reniformis
Renilla reniformis
Renilla reniformis
Human codon optimi
Clavulata sp. ant
Clavulata species
Clavulata sp. GFP
Clavulata sp. flu
Clavulata sp. chr
Discosoma striata
A. sulcata ASP499
Discosoma striata
Discosoma striata
D. striata dsFP483
D. striata dsFP483
Red fluorescent pr
Discosoma sp. "red
Discosoma species
Discosoma sp. red
Yeast optimised RF
Discosoma red fluo
H. crispa chromopr
H. crispa chromopr
H. crispa chromopr
Discosoma sp. "mag
Yeast optimised RF
H. crispa fluorese
H. crispa fluorese
H. crispa chromopr
H. crispa fluorese

DR WPI: 1999-580443/49.
 DR P-PSDB: AAY39950.
 XX
 PT New isolated Renilla mulleri, Gaussia and Pleuromamma luciferase and
 Renilla and Ptilosarcus green fluorescent protein nucleic acids -
 XX
 PS Claim 36: Page 215-216; 233pp; English.
 XX
 CC This sequence encodes a green fluorescent protein of the invention. The
 CC invention relates to Renilla mulleri, Gaussia and Pleuromamma luciferase
 CC and Renilla and Ptilosarcus green fluorescent protein (GFP) nucleic acids
 CC and proteins. The luciferases and GFPs can be used in
 CC bioluminescence-generating systems, assays, screening methods, diagnostic
 CC method and articles of manufacture. They can be expressed using
 CC e.g. bacterial, yeast, fungal, plant, insect or animal cells. The Renilla
 CC mulleri, Gaussia and Pleuromamma luciferase or Renilla or Ptilosarcus
 CC GFPs can be used in e.g. toys, cosmetics, fountains, personal care items,
 CC fairy dust, beverages, soft drinks, foods, textile products, bubbles,
 CC balloons, personal items, dentifrices, soaps, body paints, bubble bath,
 CC ink or paper products. In particular, they can be used in e.g. squirt
 CC guns, pellet guns, finger paints, foot bags, greeting cards, slimy play
 CC material, clothing, bubble making toys, bath powders, cosmetics, body
 CC lotions, gels, body powders, body creams, toothpastes, mouthwashes,
 CC soaps, body paints, bubble bath, inks, wrapping paper, gelatins, icings,
 CC frostings, greeting cards, beer, wine, champagne, soft drinks, ice cubes,
 CC ice, dry ice or fountains. The nucleic acids can also be used to produce
 CC transgenic fish and plants.
 CC
 XX
 SO Sequence 1079 BP; 375 A; 176 C; 209 G; 319 T; 0 other:
 Query Match 99.9%; Score 1077.4; DB 20; Length 1079;
 Best Local Similarity 99.9%; Pred. No. 1.1e-243;
 Matches 1078; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 601 AATTTATAGAAACAGTTTCCTACAGAGTGAATACAAAGTAGTAACCTCCAGAT 660
 DB 601 AATTTATAGAAACAGTTTCCTACAGAGTGAATACAAAGTAGTAACCTCCAGAT 660
 QY 661 GATGTCGCCGTATGACGAAGACTATCTTGAATAGAGCTTCATTTGAGCCATGTAC 720
 DB 661 GATGTCGCCGTATGACGAAGACTATCTTGAATAGAGCTTCATTTGAGCCATGTAC 720
 QY 721 ATGAATAATGGCGCTTGGGTGGCGAAGTAATTCCTGTATTAACCTAAGCTGGGAAA 780
 DB 721 ATGAATAATGGCGCTTGGGTGGCGAAGTAATTCCTGTATTAACCTAAGCTGGGAAA 780
 QY 781 TATTTATCATGTCACATGTAAGAAACATTAATGAAGTGAAGTGAAGAGATTTCT 840
 DB 781 TATTTATCATGTCACATGTAAGAAACATTAATGAAGTGAAGTGAAGAGATTTCT 840
 QY 841 TCGTATCATTTTATTCACATCGTTTGGAAAGACTTACGTAGAAACGGGGGTTCTGTT 900
 DB 841 TCGTATCATTTTATTCACATCGTTTGGAAAGACTTACGTAGAAACGGGGGTTCTGTT 900
 QY 901 GAACACATGACATGCTATTGCTCAATGACATCTATAGAAACCGACTAGATCTTA 960
 DB 901 GAACACATGACATGCTATTGCTCAATGACATCTATAGAAACCGACTAGATCTTA 960
 QY 961 CACGAATGGGTTTAAACACAGTTACATTCTTTTCCAAATGCGTTCATGTCAAAATA 1020
 DB 961 CACGAATGGGTTTAAACACAGTTACATTCTTTTCCAAATGCGTTCATGTCAAAATA 1020
 QY 1021 TAATTTTAAACATTAATCAATGTTTGTGATATGTTTGTAAAAA 1079
 DB 1021 TAATTTTAAACATTAATCAATGTTTGTGATATGTTTGTAAAAA 1079

RESULT 2
 AAF89808
 ID AAF89808 standard; DNA; 1079 BP.
 AC XX
 AC AAF89808;
 DF 23-JUL-2001 (first entry)
 XX
 DE Nucleotide sequence of Renilla green fluorescent protein.
 XX
 KW Retroviral vector; Renilla; green fluorescent protein; pgFP; rgFP; ss.
 FH Key Location/Qualifiers
 FT CDS 259..975
 FT /*tag= a
 FT /product= "green fluorescent protein (rgFP)"
 OS Renilla mulleri.
 PN WO200134824-A2.
 XX
 PD 17-MAY-2001.
 XX
 PF 10-NOV-2000; 2000WO-US30915.
 XX
 PR 10-NOV-1999; 99US-0164592.
 XX
 PA (RIGe-) RIGEL PHARM INC.
 PI Anderson D;
 XX
 DR WPI: 2001-329091/34.
 DR P-PSDB: AAB83915.
 PT Novel retroviral vector, containing gene encoding Renilla green
 PT fluorescent protein, useful as reporter for cell assays, particularly
 PT intracellular assays -
 XX
 PS Example; Fig 2; 83pp; English.

XX The specification describes a retroviral vector comprising a Renilla
CC green fluorescent protein (pGFP or rGFP) gene, pGFP and rGFP proteins
CC are useful as reporters for cell assays, particularly intracellular
CC assays including methods of screening libraries using pGFP or rGFP, and
CC for screening protein-protein, nucleic acid-protein or nucleic
CC acid-nucleic acid interactions. pGFP or rGFP proteins are also useful
CC in cellular assays, including assays for alterations in exocytosis,
CC cell cycle regulation, apoptosis, cellular proliferation and/or
CC differentiation. pGFP or rGFP proteins are also useful for elucidating
CC bioactive agents that can cause a population of cells either to move
CC out of one growth phase into another, or to arrest in a growth phase.
CC pGFP or rGFP proteins are also useful for screening bioactive agents for
CC their ability to modulate cell cycle regulation, including the activation
CC or suppression of cell cycle checkpoint pathways and ameliorating
CC checkpoint defects. The present sequence encodes rGFP.
XX
XX Sequence 1079 BP: 375 A: 176 C: 209 G: 319 T: 0 other:
SQ
Query Match 95.9%: Score 1077.4: DB 22: Length 1079:
Best local Similarity 95.9%: Pred. No. 1.1e-243:
Matches 1078: Conservative 0: Mismatches 1: Indels 0: Gaps 0:
QY 1 GGTATACACAAAGTATCGCTATCTGCAGACCATCTAGTGGATTATTGAGCGGTA 60
DB 1 GGTATACACAAAGTATCGCTATCTGCAGACCATCTAGTGGATTATTGAGCGGTA 60
QY 61 GTATTATACGTCACACCTGCTATTCGAACCAACCAACTCTTAAATAGCCACATTT 120
DB 61 GTATTATACGTCACACCTGCTATTCGAACCAACCAACTCTTAAATAGCCACATTT 120
QY 121 ACATTAATATCTAGACAGACGCTCATTTAAGTAGTAAATATATATATGATAGTA 180
DB 121 ACATTAATATCTAGACAGACGCTCATTTAAGTAGTAAATATATATATGATAGTA 180
QY 181 TACACTCTGCTTAGACAGACAGAGTGTGCAGACAGTAACCTCTTGTAAATGCAATGAA 240
DB 181 TACACTCTGCTTAGACAGACAGAGTGTGCAGACAGTAACCTCTTGTAAATGCAATGAA 240
QY 241 AGCGTCAAGAGCATATAGTACTAAACAAATATGGAAGACACTGTTTACAAAGATA 300
DB 241 AGCGTCAAGAGCATATAGTACTAAACAAATATGGAAGACACTGTTTACAAAGATA 300
QY 301 ATGTGCTATTAATGATATCTGGAAGCAATGTGAACCAACCATGTTTTCATAGGAGGT 360
DB 301 ATGTGCTATTAATGATATCTGGAAGCAATGTGAACCAACCATGTTTTCATAGGAGGT 360
QY 361 TCGGCGAAGAGCAATATTTTATTCGCAATCAACTGTTGATGATGCTGTACGAAAGGG 420
DB 361 TCGGCGAAGAGCAATATTTTATTCGCAATCAACTGTTGATGATGCTGTACGAAAGGG 420
QY 421 GCGCCACTGCTTTTGATTTGATTTGTGTACGACAGCTTTTCAATATGCAACCGTACT 480
DB 421 GCGCCACTGCTTTTGATTTGATTTGTGTACGACAGCTTTTCAATATGCAACCGTACT 480
QY 481 TTCACCAATATCCGATGATATATGATATTTTATATACATCATTTCCAGAGAGTTT 540
DB 481 TTCACCAATATCCGATGATATATGATATTTTATATACATCATTTCCAGAGAGTTT 540
QY 541 ATGTATGAACGAACTTACGTTACGAAGATGCGGACCTGTTGAAATTCCTTCAGATATA 600
DB 541 ATGTATGAACGAACTTACGTTACGAAGATGCGGACCTGTTGAAATTCCTTCAGATATA 600
QY 601 AATTATATGAACAGCAAGTCTCTACAGAGTGCATACAAAGTACGTAACCTCCAGAT 660
DB 601 AATTATATGAACAGCAAGTCTCTACAGAGTGCATACAAAGTACGTAACCTCCAGAT 660
QY 661 GATGTCCTGCTACGAGAGACTATCTTAGAATAGAGCTTCATTTGAGGCACTGTAC 720
DB 661 GATGTCCTGCTACGAGAGACTATCTTAGAATAGAGCTTCATTTGAGGCACTGTAC 720
QY 721 ATCAATATAGGCTCTTGTGCGGCAAGTAAATCTTGTCTATTAACCTCTGCGAAA 780
DB 721 ATCAATATAGGCTCTTGTGCGGCAAGTAAATCTTGTCTATTAACCTCTGCGAAA 780

DB 721 ATCAATATAGGCTCTTGTGCGGCAAGTAAATCTTGTCTATTAACCTCTGCGAAA 780
QY 781 TATTATTCATGTCACATGAAGAAACATTAATGACCTGCAAGCTGTAGTAAAGAGCTTCC 840
DB 781 TATTATTCATGTCACATGAAGAAACATTAATGACCTGCAAGCTGTAGTAAAGAGCTTCC 840
QY 841 TCGTATCATTTTATTCACATGCTTTTGGAAGAAACATCTAGTACAGCGGGGCTTCGT 900
DB 841 TCGTATCATTTTATTCACATGCTTTTGGAAGAAACATCTAGTACAGCGGGGCTTCGT 900
QY 901 GAACAGCATGACACTGCTATTTGCTCAATGACATCTATAGCAAAACCATAGATCTT 960
DB 901 GAACAGCATGACACTGCTATTTGCTCAATGACATCTATAGCAAAACCATAGATCTT 960
QY 961 CAGCAATGGGTTTAAACACAGTTACATTTCTTTTCCAAATTCGTTTCAATGTA 1020
DB 961 CAGCAATGGGTTTAAACACAGTTACATTTCTTTTCCAAATTCGTTTCAATGTA 1020
QY 1021 TAAATTTTAAACATATATATGTTTGTGATATGTTTGAATAAAAAAAAAAAAAA 1079
DB 1021 TAAATTTTAAACATATATATGTTTGTGATATGTTTGAATAAAAAAAAAAAAAA 1079
RESULT 3
AAD22198
ID AAD22198 standard; DNA: 1079 BP.
XX AAD22198;
XX 12-FEB-2002 (first entry)
XX
DE Renilla mulleri green fluorescent protein encoding DNA.
XX
KW Green fluorescent protein; GFP; bioluminescence generating system; toy;
KW Luciferase; finger paint; slimy play material; fishing lure; sparkler;
KW doll; balloon; personal care item; cosmetic; bath powder; body cream;
KW tooth paste; mouth wash; soap; body paint; ornamental transgenic plant;
KW bubble bath; fountain; fairy dust; food; gelatin; icing; frosting; beer;
KW wine; champagne; milk; soft drink; ice cube; ice; foot bag; beverage;
KW dry ice; textile; clothing; paper product; greeting card; wrapping paper;
KW ds.
XX
OS Renilla mulleri.
XX
FH Key Location/Qualifiers
FT CDS 259..975
FT /tag= a
FT /product= "Renilla mulleri green fluorescent protein"
XX
PN MO200168824-A2.
XX
PD 20-SEP-2001.
XX
PF 15-MAR-2001: 2001WO-US08277.
XX
PR 15-MAR-2000: 2000US-189691P.
XX
PA (PROL-) PROLUME LTD.
PA (BRYA/) BRYAN B J.
PI Bryan BJ, Szent-Gyorgyi C, Szczepaniak W;
PI WPI: 2002-010561/01.
DR P-PSDB: AAEI3380.
DR
PT Nucleic acids encoding Renilla reniformis green fluorescent proteins,
PT useful in diagnostic bioluminescence procedures -
XX
PS Disclosure: Page 156-157; 175pp; English.
XX
CC The patent discloses sea pansy (Renilla reniformis) green fluorescent
CC proteins (GFP) and their corresponding polynucleotides. The invention
CC also relates to sequences of the bioluminescence generating system

CC location of the polypeptide encoded by the linked polynucleotide
CC sequences, for producing a fluorescent molecular weight marker and for
CC screening for an inhibitor of a transcriptional regulatory sequence. The
CC GFP nucleic acid is also useful for monitoring the activity of a
CC transcriptional regulatory sequence, detecting a modulator such as
CC hormone, growth factor or heavy metal, especially an inhibitor of a
CC transcriptional regulatory sequence and for identifying a suitable
CC transcriptional regulatory sequence for use in recombinant expression and
CC high level protein production, such as in pre-clinical testing or in gene
CC therapy in human subjects. A cell expressing GFP as a fusion or distinct
CC polypeptide is useful for identifying cells to which a recombinant vector
CC has been introduced. The cells are preferably identified by (fluorescence
CC activated cell sorting) FACS analysis. Different coloured R.reniformis
CC GFP can be used to identify multiple cell populations in a mixed cell
CC culture or to track multiple cell types, permitting differences in cell
CC movement or migration to be visualised in real time. R. reniformis GFP
CC has superior spectral characteristics and fluorescent intensity. The
CC present sequence encodes R. reniformis GFP.
XX
XX
SQ Sequence 720 BP; 223 A; 122 C; 169 G; 206 T; 0 other;

Query Match 49.5%; Score 534.4; DB 22; Length 720;
Best Local Similarity 83.9%; Pred. No. 4e-116;
Matches 604; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 256 AAGATGAGTAAACAAATATTGAAGAACACCTGTTACAGAGTAATGCTATAGTA 315
DB 1 ATGGTGAGTAACAAATATTGAAGAACACCTGATTCAGAGAGATCATGCTTTAAAGTG 60
QY 316 AATCTGAGAGCAATGTAACAAACCATGTTTATCAATGAGAGGTTGGCCAAAGGCAAT 375
DB 61 AATCTGAGAGCAATGTAACAAACCATGTTTATCAATGAGAGGTTGTGAAAGCAAAAT 120
QY 375 ATTTTATTCGGCAATCACTGATTCAGATTCGTCACGAAAGGGCCGACATGCTTTT 435
DB 121 ATTTTATTCGGCAACCACTGGTTCAGATTCGTCACAAAGGGGTCGCTTCATTT 180
QY 436 GCATTTGATATTGTCACCAAGCTTTTCAATATGGCAACCGCTATTACAGAAATATCCG 495
DB 181 GCATTTGATATTGTCACCAAGCTTTTCAATATGGCAACCGCTATTACAGAAATATCCG 240
QY 496 AATGATATATCAGATTTATTTATACATCATTTCCAGCAGATTTATATGAACGACA 555
DB 241 GAGCATATATCAGATTTTATATCAATCATTTCCACGGGATTTGATACGAACGAC 300
QY 556 TTACGTTAGCAAGATGGCGGACCTGTTGAATTCGTTCAATATATTAATTAGAAAGAC 615
DB 301 TTGCGTTAGCAAGATGGTGAGCTGTTGAATTCGTTCAATATTAATTATGAGAGAC 360
QY 616 AAGTCTCTACAGAGTGCATACAAAGTAGTAACCTCCAGATGATGGTCCGTCATG 675
DB 361 ATGTTTGTCTACAGAGTGCATATTAAGTAGTAACCTCCGATATGATGTCATGATG 420
QY 676 CAGAAGCATATCTTAGCATATGAGCCCTTCATTTGAAGCCATGTACATGAATAATGGCGTC 735
DB 421 AAGAACAACATCAGAGATATACCAACCTTCGTTCAAGCTTGTATATATGACGATGGCGTC 480
QY 736 TTGTCGGCCCAAGCAATCTTGTCTATTAACCTTAACCTTCGGAATATTTATCATGTCAC 795
DB 481 TTGTCGGCCCAAGCAATCTTGTCTATTAACCTTCGGAATATTTATCTGTGTCAC 540
QY 796 ATGAAGCACTAATTAAGTGAAGAGTGTAGTAAGAGATTCCTTCGTTCAATTTATTT 855
DB 541 ATGAAGCACTAATTAAGTGAAGAGTGTAGTAAGATTCCTTCGGAATATTCATTTTCAT 600
QY 856 CAACATCTGTTTGAAGAAAGACTTACGTAAGAGCGGGGCTTCTTGAACGATGAGACT 915
DB 601 CAACATCTGTTTGAAGAAAGACTTACGTAAGAGCGGGGCTTGTGTGCAACGACGACG 660
QY 916 GCATATGCTCAATGAATGACATATATGAAGAAACCACTGAGATCCTTACAGCAATGGTTAA 975
DB 661 GCCATTTCCTCACTGACATCGCTGGGGAAACCACTTGATCCTTACAGCAATGGCTTTAA 720

RESULT 5
ID AB073693 standard; DNA: 720 BP.
XX
XX AB073693:
XX
XX 07-OCM-2002 (first entry)
XX
XX Ren11la reniformis green fluorescent protein nucleotide SEQ ID NO:1.
DE
XX Ren11la reniformis; green fluorescent protein; GFP; fluorescence;
KM fusion protein; intramolecular dimer fluorescent protein; IDFP; FACS;
KM multimeric protein; fluorescence activated cell sorting; cell population;
KM viral vector infection; fluorescence resonance energy transfer; FRET;
KM transgene expression; protein:protein interaction; gene: ds.
XX
XX Ren11la reniformis.
OS

XX
XX Key Location/Qualifiers
FH
FT 1.720
FT CDS
FT /tag= a
FT /product= "green fluorescent protein"
FT /transl_except= (pos:1..6,aa:Met)
FT /transl_except= (pos:358..360,aa:Gln)
XX
XX MO200248174-A2.
XX
XX 20-JUN-2002.
XX
XX 13-DEC-2001; 2001WO-US486590.
XX
XX 15-DEC-2000; 2000US-256121P.
XX
XX (STRA-) STRATAGENE.
XX
XX Davis RW, Valliancourt P;
XX
XX WPI: 2002-583482/62.
XX
XX P-PSDB: ABP51820.
XX
XX

PT Novel recombinant fusion polypeptide which is fluorescent when excited,
PT comprising first polypeptide peptide-bonded to second polypeptide, the
PT polypeptides being found in nature as monomers of a multimeric protein
PT
XX
XX Disclosure: Fig 1; 59pp; English.

XX
XX The present invention describes a recombinant fusion polypeptide
XX (intramolecular dimer fluorescent protein (IDFP)) (I) comprising a first
XX polypeptide peptide-bonded to a second polypeptide, where the first and
XX second polypeptides are found in nature as monomers of a multimeric
XX protein and the first and second polypeptides are not fluorescent donor
XX and acceptor to each other, and (I) is fluorescent when excited. (I) is
XX useful for monitoring the interaction of two polypeptides of interest
XX which involves contacting a first polypeptide and the second polypeptide.
XX (I) is also useful for screening for a compound that modulates the
XX interaction of first and second member of specific binding pair which
XX involves contacting a first polypeptide and a second polypeptide in the
XX presence and absence of candidate modulator. (I) can be used as reporter
XX genes to monitor the activity of promoter sequences to investigate the
XX cellular localisation of fusion proteins, to mark cellular proteins for
XX fluorescence activated cell sorting (FACS) analyses of cell population,
XX to monitor viral vector infection, to monitor transgene expression
XX in vivo or in culture, and to monitor protein:protein interactions both
XX in vivo and in vitro. (I) is suitable for applications that rely on
XX fluorescence resonance energy transfer (FRET). The present sequence
XX encodes Ren11la reniformis green fluorescent protein (GFP), which is
XX given in the exemplification of the present invention.

SQ Sequence 720 BP; 223 A; 122 C; 169 G; 206 T; 0 other;
Query Match 49.5%; Score 534.4; DB 24; Length 720;

Best Local Similarity	83.9%	Pred. NO.	4e-116;
Matches	604;	Conservative	0;
		Mismatches	116;
		Indels	0;
		Gaps	0

QY	256	AAATGATGATGAACCAATATTTGSAAGACCTGGTTTACAAAGATGAATTCGTATTAAGA	315
Db	1	ATGTGATGATGAACCAATATTTGSAAGACCTGGTTTACAAAGATGAATTCGTATTAAGA	60
QY	316	AAATGATGATGAACCAATATTTGSAAGACCTGGTTTACAAAGATGAATTCGTATTAAGA	375
Db	61	AAATGATGATGAACCAATATTTGSAAGACCTGGTTTACAAAGATGAATTCGTATTAAGA	120
QY	376	AAATGATGATGAACCAATATTTGSAAGACCTGGTTTACAAAGATGAATTCGTATTAAGA	435
Db	121	AAATGATGATGAACCAATATTTGSAAGACCTGGTTTACAAAGATGAATTCGTATTAAGA	180
QY	436	AAATGATGATGAACCAATATTTGSAAGACCTGGTTTACAAAGATGAATTCGTATTAAGA	495
Db	181	AAATGATGATGAACCAATATTTGSAAGACCTGGTTTACAAAGATGAATTCGTATTAAGA	240
QY	496	AAATGATGATGAACCAATATTTGSAAGACCTGGTTTACAAAGATGAATTCGTATTAAGA	555
Db	241	AAATGATGATGAACCAATATTTGSAAGACCTGGTTTACAAAGATGAATTCGTATTAAGA	300
QY	556	AAATGATGATGAACCAATATTTGSAAGACCTGGTTTACAAAGATGAATTCGTATTAAGA	615
Db	301	AAATGATGATGAACCAATATTTGSAAGACCTGGTTTACAAAGATGAATTCGTATTAAGA	360
QY	616	AAATGATGATGAACCAATATTTGSAAGACCTGGTTTACAAAGATGAATTCGTATTAAGA	675
Db	361	AAATGATGATGAACCAATATTTGSAAGACCTGGTTTACAAAGATGAATTCGTATTAAGA	420
QY	676	AAATGATGATGAACCAATATTTGSAAGACCTGGTTTACAAAGATGAATTCGTATTAAGA	735
Db	421	AAATGATGATGAACCAATATTTGSAAGACCTGGTTTACAAAGATGAATTCGTATTAAGA	480
QY	736	AAATGATGATGAACCAATATTTGSAAGACCTGGTTTACAAAGATGAATTCGTATTAAGA	795
Db	481	AAATGATGATGAACCAATATTTGSAAGACCTGGTTTACAAAGATGAATTCGTATTAAGA	540
QY	796	AAATGATGATGAACCAATATTTGSAAGACCTGGTTTACAAAGATGAATTCGTATTAAGA	855
Db	541	AAATGATGATGAACCAATATTTGSAAGACCTGGTTTACAAAGATGAATTCGTATTAAGA	600
QY	856	AAATGATGATGAACCAATATTTGSAAGACCTGGTTTACAAAGATGAATTCGTATTAAGA	915
Db	601	AAATGATGATGAACCAATATTTGSAAGACCTGGTTTACAAAGATGAATTCGTATTAAGA	660
QY	916	AAATGATGATGAACCAATATTTGSAAGACCTGGTTTACAAAGATGAATTCGTATTAAGA	975
Db	661	AAATGATGATGAACCAATATTTGSAAGACCTGGTTTACAAAGATGAATTCGTATTAAGA	720
RESULT 6			
DD	AA227548	standard: DNA; 1104 bp.	
XX	AA227548:		
XX	13-DEC-1999	(first entry)	
DE	Ptilosarcus green	fluorescent protein coding sequence.	
XX	Luciferase; green	fluorescent protein; GFP; screening assay; diagnosis;	
KW	bio luminescence-generating system; toy; cosmetic; fairy dust; beverage;		
KM	body paint; squirt gun; balloon; slimy play material; soap; toothpaste;		
KW	ds.		
XX	Ptilosarcus gunneyi.		
OS	MO9949019-A2.		
XX	30-SEP-1999.		


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DT 12-FEB-2002 (first entry)
XX
DE Ptiliosarcus gurneyi green fluorescent protein encoding DNA #1.
XX
KM Green fluorescent protein: GFP: bioluminescence generating system: toy:
KM Luciferase: finger paint: slimy play material: fishing lure: sparkler:
KM doll: balloon: personal care item: cosmetic: bath powder: body cream:
KM tooth paste: mouth wash: soap: body paint: ornamental transgenic plant:
KM bubble bath: fountain: fairy dust: food: gelatin: icing: frosting: beer:
KM wine: champagne: milk: soft drink: ice cube: ice: foot bag: beverage:
KM dry ice: textile: clothing: paper product: greeting card: wrapping paper:
KM
XX
OS Ptiliosarcus gurneyi.
XX
FH Key Location/Qualifiers
FT 34..750
FT CDS /tag=a
FT /product="P. gurneyi green fluorescent protein"
XX
PN MO200168824-A2.
XX
PD 20-SEP-2001.
XX
PF 15-MAR-2001: 2001WO-US08277.
XX
PR 15-MAR-2000: 2000US-189691P.
XX
PA (PROL-) PROLUME LTD.
PA (BRYA/) BRYAN B J.
PI Bryan BJ, Szent-Gyorgyi C, Szczepaniak W:
XX
PI WPI: 2002-010561/01.
XX
DR P-PSDB: AAE13386.
XX
XX Nucleic acids encoding Renilla reniformis green fluorescent proteins,
XX useful in diagnostic bioluminescence procedures -
XX
PS Disclosure: Page 172-173; 175pp: English.
XX
XX
XX The patent discloses sea pansy (Renilla reniformis) green fluorescent
XX proteins (GFP) and their corresponding polynucleotides. The invention
XX also relates to sequences of the bioluminescence generating system
XX (e.g. luciferase). R. reniformis GFP are used in diagnostic methods
XX and in the production of novelty items such as toys (e.g. squirt gun,
XX pellet gun, toy "halloween" eggs, toy cigarettes, board/card game
XX toys), finger paints, slimy play material, bubbles in bubble making
XX toys, fishing lures, dolls, sparklers, magic wand toys, balloons,
XX personal care item (e.g. cosmetic, bath powders, body creams, tooth
XX pastes, mouth wash, soaps, body paints, bubble bath), ornamental
XX transgenic plants, fountain, fairy dust, food (gelatin, icings,
XX frosting, beers, wine, champagne, milk, soft drinks, ice cubes, ice,
XX dry ice, beverage), textile (foot bag, clothing) and/or paper product
XX (greeting cards, wrapping paper). The present sequence is a DNA
XX encoding Ptiliosarcus gurneyi green fluorescent protein.
XX
SQ Sequence 1104 BP: 360 A; 215 C; 237 G; 292 T; 0 other:
XX
Query Match 36.4%; Score 392.6; DB 24; Length 1104;
Best Local Similarity 71.3%; Pred. No. 9, 5e-83;
Matches 518; Conservative 0; Mismatches 209; Indels 0; Gaps 0;
XX
OY 252 AGATAGATGACGTAACAAATATTGAAGACACTGTTGTTCAAGAGTATGTCGTTAA 311
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27 AGACAAATGACCGACGACGATTTAAAGACACTGACGTAAGACATTAATGTCGCAAA 86
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 312 AGTAATCTGGAAGATTTGTAACAACATGTTTACATGAGAGTGGCGCAAGG 371
XX || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 87 AGCTAGCGTTGAAGGATCTGAACAATCAGCTTTTTCATGATGAAAGATTGGAAAAGG 146
XX || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 372 GAATATTTTATTTGGGCAATTCAGTGGTTCGATTCGTGCACGAAAGGGGCCACATGCC 431
XX || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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DB 147 CAATGATATTATTGGAACCAATTGATGCAAAATCCGGGTTACAAAGGAGGTCCTTGCC 206
OY 432 TTTTGATTTGATATTGTCGACACGACTTTTCAATATGCAACCGTACTTTTCAGCAATA 491
XX || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 207 ATTGCGCTTTCGATATTGTTTCATACCTTTTCCAAATACGGGAATCGCATTCACGAAATA 266
OY 492 TCCGATGATATATATTCAGATTATTTATACATCATTTTCAGAGAGTTTATGATGACGA 551
XX || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 267 CCGAGACGACATTTGGCGGACTACTTTGTTCAATCATTTCCCGGCTGGATTTTTCAGCAAAAG 326
OY 552 AACATTACGTTACGAAGATGGCGGACTTGTGAATTCGTTGAGATATATAATTTAATAGA 611
XX || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 327 AATCTACGCTTTGAGAGATGGCGCCATTTGTGACATTGCTTCAGATATATAAGTTAGAGA 386
OY 612 AGACAGTTCGTTACAGACTGCAATACAAAGTACTTAATCTCCGAGATGTCCTCGT 671
XX || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 387 TGATTAAGTTCCACTCAAGAGTGAGATAGAGCAACGCTTTCCTAGTAACGACGCCGT 446
OY 672 CATGACGAAGACTATCTTGGAAATAGAGCCCTTCAATTTGAAGCCATGATGATAATAGG 731
XX || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 447 GATGCAAAAAGCCATCTCGCATGAGCCATCGTTTGAGTGCTTACATGACACGCG 506
OY 732 CGTCTTGGTCGGGGAAGTAAATCTTCTCTAATAACTTAACCTTGGAATAATATTATTCATG 791
XX || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 507 CGTTCTGTGGCGGAGTAGATCTCGTTTACAAACTCGAGTCAAGGAACTATTACTGCTG 566
OY 792 TCACATGAAAACATTTAATGAGTCGAAGGTGATGATGAAGGACTTTCCTTCATATTT 851
XX || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 567 CCACATGAAAACGTTTACAGATCGACAAAGGTGAGGAAGAAATTCGCCGAATATCATCTT 626
OY 852 TATTCAACATCGTTTGAAGAAAGACTTACGTAGAGAGCGGGCTTGTGAACAGCATGA 911
XX || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 627 TATTCATCATCTGCTGTGAGAAACCTACGTGGAAGAGAACGCTTGTGTAACAACACGA 686
OY 912 GACTGCTATTTGCTCAAAATGACATCTATAGCAAAAACCATAGCATTCCTTACCAATGGCT 971
XX || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 687 GACGGCCATTTGACACACTACCAATTTGAAAACCTTGCGCTCCCTTCATGAAATGGCT 746
OY 972 TTAAACA 978
XX || | | |
DB 747 GTAGAAA 753
XX
RESULT 9
AA227549
ID AA227549 standard: DNA: 1279 BP.
XX
AC AA227549:
XX
DT 13-DEC-1999 (first entry)
XX
DE Ptiliosarcus green fluorescent protein coding sequence.
XX
XX Luciferase: green fluorescent protein: GFP: screening assay: diagnosis:
XX bioluminescence-generating system: toy: cosmetic: fairy dust: beverage:
XX body paint: squirt gun: balloon: slimy play material: soap: toothpaste:
XX ds.
XX
OS Ptiliosarcus gurneyi.
XX
PN WO9949019-A2.
XX
PD 30-SEP-1999.
XX
PF 26-MAR-1999: 99WO-US06698.
XX
PR 27-MAR-1998: 98US-0075624.
PR 15-JUN-1998: 98US-0089367.
PR 01-OCT-1998: 98US-0102939.
XX
PA (PROL-) PROLUME LTD.
PA (BRYA/) BRYAN B J.
XX

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PI	Bryan BJ, Szent-Gyorgyi C:	
DR	WPI: 1999-580443/49.	
XX	P-PSDB: AAY35951.	
PT	New isolated Renilla mulleri, Gaussia and Pleuromamma luciferase and	
PT	Renilla and Ptilosarcus green fluorescent protein nucleic acids -	
XX	Claim 36; Page 231-232; 233pp; English.	
XX	This sequence encodes a green fluorescent protein of the invention. The	
CC	invention relates to Renilla mulleri, Gaussia and Pleuromamma luciferase	
CC	and Renilla and Ptilosarcus green fluorescent protein (GFP) nucleic acids	
CC	and proteins. The luciferases and GFPs can be used in	
CC	bioluminescence-generating systems, assays, screening methods, diagnostic	
CC	method and articles of manufacture. They can be expressed using	
CC	e.g. bacterial, yeast, fungal, plant, insect or animal cells. The Renilla	
CC	mulleri, Gaussia and Pleuromamma luciferase or Renilla or Ptilosarcus	
CC	GFPs can be used in e.g. toys, cosmetics, fountain, personal care items,	
CC	fairy dust, beverages, soft drinks, foods, textile products, bubbles,	
CC	balloons, personal items, dentifrices, soaps, body paints, bubble bath,	
CC	ink or paper products. In particular, they can be used in e.g. squirt	
CC	guns, pellet guns, finger paints, foot bags, greeting cards, slimy play	
CC	material, clothing, bubble making toys, bath powders, cosmetics, body	
CC	lotions, gels, body powders, body creams, toothpastes, mouthwashes,	
CC	soaps, body paints, bubble bath, inks, wrapping paper, gelatins, icings,	
CC	flourings, greeting cards, beer, wine, champagne, soft drinks, ice cubes,	
CC	ice, dry ice or fountains. The nucleic acids can also be used to produce	
CC	transgenic fish and plants.	
XX		
S0	Sequence 1279 BP: 449 A: 234 C: 263 G: 333 T: 0 other:	
	Query Match 36.3%; Score 391.6; DR 20; Length 1279;	
	Best Local Similarity 71.2%; Pred. No. 1.7e-82;	
	Matches 517; Conservative 0; Mismatches 209; Indels 0; Caps 0	
QY	253 GATAAGATGAGTAACAAATATTGAAAGAACACTTTGTTACAAGAACTAATGTCGTATAA 312	
Db	1 GACAAATATGACCCGACAGCTATTAAAGAACACTGCGACTGAAGACATTAATTCGCCCAA 60	
QY	313 GTAATTCGGAAGGAAATGTTAAACCAACCTGTTTACATAGAGCGTTGGCCCAAGG 372	
Db	61 GCTACCGTTGAAGGAAATCTGAACATATCAGTTTTCATGAGAAAGATTGGAAAAGG 120	
QY	373 AATATTTATTCGGCAATCACTGCTGAGTTTCGTTCAGCAAAAGGCGCCAGCTGCC 432	
Db	121 AATGATATTATTGGAACCAATTGATTCGAATCCGGCTTACAAAGGAGAGCTCCGTTGCC 180	
QY	433 TTTCGATTTCATATTGTGTGTCACCACTTTCAATATGCAACCGTACTTTCAGCAATAT 492	
Db	181 TTTCGCTTCGCAATTCGTTTCATACCTTTCCAAATACGGGAATTCGCCACTTTCAGCAATAT 240	
QY	493 CCGAATGATATATTCAGATATTATTATACATCATTTCCGCAAGAGATTATGTAAGCA 552	
Db	241 CCAGACGACATTTGCGGACTACTTTGTTCAATATTTCCGCGTGGAATTTTCTACGGAAG 300	
QY	553 ACATTACGTTACGAAGATGCGGAGCTTGTGAAATTCGTTGAGATATAATTAATGAAG 612	
Db	301 AATTCAGCTTTGAAGATGCGGCCACTTTGTGACATTCGTTGAGATATAAGATTAGAAGAT 360	
QY	613 GACAAAGTTCGTTACAGAGTGCATATACAAAGGTACTACTTCCAGATGATGCTCCGCT 672	
Db	361 GATAGTTTCGCAATCAAAAGTGAGATATAGAGCAACGCTTTCCCTTAGTAAACGACCGCTG 420	
QY	673 ATCCGAGAGACTATTTAGCAATACAGCCTPATTTTGAAGCAATGATGATGTAATATGGC 732	
Db	421 ATGCAAAAAGCATCTCTCGGCATGAGGCCATTCGTTTGAAGTGGCTACATGGAACACCGGC 480	
QY	733 GTCTTGTGTCGGGCAAGTAACTCTGCTATAAAGTAAACTCTGGCAAAATATTATTCATG 792	
Db	481 GTTCTGTGCGGGAAGTAGATCTCGTTTACAAAGTCGACTCAAGGAAGATATTATTCGTCGC 540	
QY	793 CACATGAACACATTATAGAGTGCAGAAAGGTGATGAAGGACTTTCCTTCGTATCATTTT 852	

Db	541	CACATGAAACGTTTACAGATCCAAAGGTGGAGTGAAAGAAATCCCGGAAATATACCTT	600
Qy	853	ATTCAACATTCCTTTPGGAAGAACCTTACGTGTAAGACGGGGGTTGGTTGACAGCATGAG	912
Db	601	ATTCATCATCTCTCTGGAGAAACCTTACGTGTAAGAAAGAACTTGTGTGAACACACGAG	660
Qy	913	ACTGCTATTGCTCAATGACATCTATAGCAAAACCACTAGCATCCGTTCACCAATGGCTT	972
Db	661	ACGGCAATTCGACACAGTACACCAATTTGGAAAACCTCTGGGCTCCCTTCATGAAATGGGTG	720
Qy	973	TAACA 978	
Db	721	TAGAAA 726	
RESULT 10			
AAAF89810			
ID	AAE89810	standard; DNA; 1279 BP.	
XX	AAF89810;		
AC	23-JUL-2001	(first entry)	
XX			
DE	Nucleotide sequence of a green fluorescent protein.		
XX	Retroviral vector; Renilla; green fluorescent protein; pGFP; rGFP; ss.		
KW	Ptilosarcus gurneyi.		
OS			
XX			
FH	Key	Location/Qualifiers	
FT	CDS	7..723	
FT		/*tag= a	
FT		/product= "green fluorescent protein (pGFP)"	
XX	WO200134824-A2.		
PN	17-MAY-2001.		
PD	10-NOV-2000; 2000WO-US30915.		
XX	10-NOV-1999; 99US-0164592.		
PR	(RIGE-) RIGEL PHARM INC.		
XX	Anderson D;		
P1	WPI: 2001-329091/34.		
DR	P-PSDB: AAB83917.		
XX	Novel retroviral vector, containing gene encoding Renilla green		
PT	fluorescent protein, useful as reporter for cell assays, particularly		
PT	intracellular assays -		
XX	Example; Fig 3B; 83pp; English.		
XX	The specification describes a retroviral vector comprising a Renilla		
CC	green fluorescent protein (pGFP or rGFP) gene, pGFP and rGFP proteins		
CC	are useful as reporters for cell assays, particularly intracellular		
CC	assays including methods of screening libraries using pGFP or rGFP, and		
CC	for screening protein-protein, nucleic acid-protein or nucleic		
CC	acid-nucleic acid interactions. pGFP or rGFP proteins are also useful		
CC	in cellular assays, including assays for alterations in exocytosis,		
CC	cell cycle regulation, apoptosis, cellular proliferation and/or		
CC	differentiation. pGFP or rGFP proteins are also useful for elucidating		
CC	bioactive agents that can cause a population of cells either to move		
CC	out of one growth phase into another, or to arrest in a growth phase.		
CC	pGFP or rGFP proteins are also useful for screening bioactive agents for		
CC	their ability to modulate cell cycle regulation, including the activation		
CC	or suppression of cell cycle checkpoint pathways and ameliorating		
CC	checkpoint defects. The present sequence encodes pGFP.		
XX	Sequence 1279 BP; 449 A; 234 C; 263 G; 333 T; 0 other;		

0Y	553	ACATTACGTTACGAAGATGC ⁷ GCAGCTTGTTGAAATTGCTTCAGATAT ¹ AAATTAA ¹ TAGAA	512
Db	301	ATCTCTCCTTTGAAGATGGCGCCATTGTTGACATTCGTTCCGATTA ¹ TAGAT	360
0Y	613	GACAGCTTCGCTCTACAGAGTTGAAATACAAAGCTGTAACTTCCTCCGATAGATGGTCCGCTC	672
Db	361	CATTAGCTTCACATAAAGTGGAGCTATAGAGCAACGGTTCCTTACGTAAACGACCCGTG	420
0Y	673	ATGCGAAGACTATCTTAAGAAATAGAGCTTCATTGAAGCCATGTACATGAAT ¹ ATAGC	732
Db	421	ATGCAAAAAAGCCATCTCGCGCATGGAGCCATCGTTTGAAGTGCTCTCATGAACAGCGC	480
0Y	733	GCTCTGTCGGCGGAAGTATTTCTTGCTATAAACTAAAGCTGGGAATAT ¹ TATAT	792
Db	481	GTTCTGGTGGGGGAAGTAGATGTGTTTACAAAGCTCGAGTAGGAGAACTAT ¹ ACTGTGC	540
0Y	793	CACATGAAGACATTATGATGACTCGAAAGGTGACTAAAGCAAGTTCTCTGTATCATTT	852
Db	541	CACATGAAGACGTTTACAGATCCAAAGGTGGAGTGAACAAATTTCCGCGAATATCA ¹ TT	600
0Y	853	ATTTCACATTCGTTTGGAAAGACTTACGTTACAGACGGGGGTTGCTTGAACAGCATGAG	912
Db	601	ATCCATCAATCTCTCGAAGAAAGCTACCTGGAGAAAGAGAAAGCTTCGTCGAACAACAGAG	660
0Y	913	ACTGCTATTTGCTCAAAATGACATCTATAGAAAGCACTTAGATCTCTACAGCAATGGCT	972
Db	661	ACGGCCATTGGACAACTGATCCATCAATTTGGAAAGCTCTGGGGTCCCTTCAATGAATGGGTG	720
0Y	973	TAAACA	978
Db	721	TAGAAA	726

RESULT 12	
AASt4038	
ID	AASt4038 standard; cDNA: 720 bp.
XX	
AC	AASt4038:
XX	
DT	18-DEC-2001 (first entry)
XX	
DE	R. reniformis humanised cDNA encoding Green fluorescent protein, GFP.
XX	
KW	Green fluorescent protein; GFP; ss: gene therapy; FACS analysis; mutant
XX	protein-protein interaction; Fluorescence activated cell sorting.
OS	Renilla reniformis.
XX	Synthetic.
XX	
EH	Key
FT	location/Qualifiers
FT	1..720
FT	/*tag= a
FT	/product= "GFP"
FT	/transl_except= (pos:391..393,aa:Ser)
FT	replace (9,T)
FT	/*tag= b
FT	replace (12,A)
FT	/*tag= c
FT	replace (15,A)
FT	/*tag= d
FT	replace (18..19,AT)
FT	/*tag= e
FT	replace (30,T)
FT	/*tag= f
FT	replace (33..34,AT)
FT	/*tag= g
FT	replace (49..51,TCG)
FT	/*tag= h
FT	replace (54,T)
FT	/*tag= i
FT	replace (57,A)
FT	/*tag= j

FT	mutation	replace (63,T)
FT	mutation	/*tag= k replace (69,A)
FT	mutation	/*tag= i replace (72,T)
FT	mutation	/*tag= m replace (75,A)
FT	mutation	/*tag= n replace (78,T)
FT	mutation	/*tag= o replace (84,T)
FT	mutation	/*tag= p replace (87,T)
FT	mutation	/*tag= q replace (96,A)
FT	mutation	/*tag= r replace (102,A)
FT	mutation	/*tag= s replace (105,T)
FT	mutation	/*tag= t replace (108,T)
FT	mutation	/*tag= u replace (111,A)
FT	mutation	/*tag= v replace (114,A)
FT	mutation	/*tag= w replace (117,A)
FT	mutation	/*tag= x replace (120,T)
FT	mutation	/*tag= y replace (123, 124,TT)
FT	mutation	/*tag= z replace (126,A)
FT	mutation	/*tag= aa replace (132,A)
FT	mutation	/*tag= ab replace (138,T)
FT	mutation	/*tag= ac replace (150,T)
FT	mutation	/*tag= ad replace (153,C)
FT	mutation	/*tag= ae replace (156,A)
FT	mutation	/*tag= af replace (159,A)
FT	mutation	/*tag= ag replace (162,G)
FT	mutation	/*tag= ah replace (165,T)
FT	mutation	/*tag= aj replace (168,G)
FT	mutation	/*tag= ak replace (171,T)
FT	mutation	/*tag= al replace (174,G)
FT	mutation	/*tag= am replace (177,T)
FT	mutation	/*tag= an replace (180,T)
FT	mutation	/*tag= ao replace (183,A)
FT	mutation	/*tag= ap replace (186,T)
FT	mutation	/*tag= aq replace (189,T)
FT	mutation	/*tag= ar replace (192,T)
FT	mutation	replace (195, 198,CTCA
FT	mutation	/*tag= as replace (201,A)
FT	mutation	/*tag= at replace (204,T)

FT mutation /tag= au
FT replace (210,A)
FT /tag= av
FT replace (222,T)
FT /tag= aw
FT replace (225,A)
FT /tag= ax
FT replace (231,G)
FT /tag= ay
FT replace (234,A)
FT /tag= az
FT replace (240,G)
FT /tag= ba
FT replace (249..252,ATCA)
FT /tag= bb
FT replace (258,T)
FT /tag= bc
FT replace (261,T)
FT /tag= bd
FT replace (264,A)
FT /tag= be
FT replace (267..270,ATCA)
FT /tag= bf
FT replace (273,T)
FT /tag= bg
FT replace (276,A)
FT /tag= bh
FT replace (279,G)
FT /tag= bi
FT replace (282,A)
FT /tag= bj
FT replace (285,T)
FT /tag= bk
FT replace (288,A)
FT /tag= bl
FT replace (294..295,AA)
FT /tag= bm
FT replace (297,A)
FT /tag= bn
FT replace (300..301,GT)
FT /tag= bo
FT replace (306,T)
FT /tag= bp
FT replace (312,A)
FT /tag= bq
FT replace (315,T)
FT /tag= br
FT replace (318,T)
FT /tag= bs
FT replace (321,T)
FT /tag= bt
FT replace (327,T)
FT /tag= bu
FT replace (330,A)
FT /tag= bv
FT replace (336..339,TTCA)
FT /tag= bw
FT replace (342,T)
FT /tag= bx
FT replace (345,A)
FT /tag= by
FT replace (348..349,TT)
FT /tag= bz
FT replace (351,A)
FT /tag= ca
FT replace (266,T)
FT /tag= cb
FT replace (369,C)
FT /tag= cc
FT replace (373,A)
FT /tag= cd
FT replace (375,A)
FT /tag= ce

FT mutation replace (381,A)
FT /tag= cf
FT replace (384,T)
FT /tag= cg
FT replace (387,A)
FT /tag= ch
FT replace (390..391,TA)
FT /tag= ci
FT replace (393,T)
FT /tag= cj
FT replace (402,G)
FT /tag= ck
FT replace (405,T)
FT /tag= cl
FT replace (408,T)
FT /tag= cm
FT replace (411,T)

Query Match 31.1%; Score 336; DB 22; Length 720;

Best Local Similarity 66.7%; Pred. No. 1,7e-69;

Matches 480; Conservative 0; Mismatches 240; Indels 0; Gaps 0;

QY 256 AAGATGATGAACAAATATTGAAGACACTGTTTACAAGAAGTAATGCTGATAAAGTA 315
1 ATGCTGAGCAGACAGATCCTGAAGAACACCGGCTGCAGAGATCATGAGCTTCAAGTGTG 60
QY 316 AATCTGAAGGAATTTAAACAAACCATGTTTATACATGAGAGGTTGGCGCAAGGGAAT 375
61 AACCTGGAGGGCGTGTGAACACACAGCTTCACATGAGAGGCTGGCGCAAGGGAAC 120
QY 376 ATTTATTCGGCAATCAACAGCTGTTAGATTCTGTCCAGAAAGGGCCCCACTGCCTTTT 435
121 ATCTCTTTCGGCAACACAGCTGTTGATTCGGGATTCGGGTACCAAGGGGCCCCCTGCCTTC 180
QY 436 GCATTGATATTTGTCTACCAGCTTTTCAATATGCAACCGTACTTTCAGGAATATCCG 495
181 GCCTTCAGATCCTGAGCCCGCCCTTCAGTACGGCAACCGACCTTTCACCAAGTACCCC 240
QY 496 AATGATATATTCAGATTATTTATACAAATCATTTCCAGCGAATTTATGATGACGAACA 555
241 GAGGACATCAGCGACTTCTTCATCCAGACCTTCCCGGCTTCGTGTACGAGGCGCAC 300
QY 556 TTACGTTACGAAGATGCGGACTTGTGAATTCGTTACGATATAAATTTAATAGAAAGAC 615
301 CTGCGCTACGAGAGCGCGGCTGTGTGAGATCCGAGGACATCAACCTGATCGAGGAG 360
QY 616 AAGTTCGTACAGAGTCGAATACAAAGGTAGTAACTTCCAGANTGATGTCGCCGTATG 675
361 ATGTTGCTGATACCGCGTGAAGTACAAAGGCGCGCAACTTCCCAACGACGCGCCGTGATG 420
QY 676 CAGAAGCTATCTTAGCAATAGAGCCTTCATTGGAAGCATGTACATGANTATAGCGCTC 735
421 AAGAAGACCATCACCGGCTGCAGGCCAGCTTCGAGGTGTGATCAATGGAACGACGCGTG 480
QY 736 TTGTCGGCGAAGTAATTTCTGTCTATAAATTAACCTGGGAATATTTATTCATGTCAC 795
481 CTGTGGGCGCAGTGTATCTGTGTACCGGCTGACAGGCGGAAGTTCTACAGCTCCGAC 540
QY 796 ATGAANAACATTAATGAAGTCGAAAGGTGTAGTAAGAGAGTTCCCTGATCATTTTAT 855
541 ATGCGCACCTTGATGAAGAGCAAGGGCGTGTGAAGAGACTTCCCGCATCACCTTCATC 600
QY 856 CAACATCGTTTGGAAAGAAGCTTAGAAGACGGGGGCTTCGTTAAGCATGAGACT 915
601 CAGCACCGCTGGAGAAGACTTACGTGAGAGAGGGCGCTTCGTGAGACGACGAGACC 660
QY 916 GCATTATGCTCAATGACATCTATAGAAAACCACTAGATTCCTTACCAATAGGCTTTAA 975
661 GCCATGCCCAGCTGACCAAGCTGGGCAAGCCCTTGGCAGCCTGACAGATGGGTGTA 720

RESULT 13
ABQ73694

ID AB073694 standard; DNA: 720 BP.
XX
AC AB073694:
XX
DT 07-OCT-2002 (first entry)
XX
DE Humanised Renilla reniformis GFP nucleotide SEQ ID NO:3.
XX
KM Renilla reniformis: green fluorescent protein; GFP: fluorescence:
KM fusion protein; intramolecular dimer fluorescent protein; IDFP; FACS:
KM multimeric protein; fluorescence activated cell sorting; cell population;
KM viral vector infection; fluorescence resonance energy transfer; FRET;
KM transgene expression; protein:protein interaction; humanised; gene; ds.
XX
OS Renilla reniformis.
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT 1..720 /tag= a
FT CDS /product= "humanised green fluorescent protein"
FT /transl_except= (pos:391..395,aa:Ser)
XX
PN W0200248174-A2.
XX
PD 20-JUN-2002.
XX
PF 13-DEC-2001: 2001WO-US48690.
XX
PR 15-DEC-2000: 2000US-256121P.
XX
PA (STRA-) STRATAGENE.
XX
PI Davis RW, Vallancourt P;
XX
DR WPI: 2002-583482/62.
XX
DR P-PSDB: ABP51821.
XX
PT Novel recombinant fusion polypeptide which is fluorescent when excited,
PT comprising first polypeptide peptide-bonded to second polypeptide, the
PT polypeptides being found in nature as monomers of a multimeric protein
PT
XX
PS Disclosure; Fig 3: 59pp; English.
XX
CC The present invention describes a recombinant fusion polypeptide
CC (intramolecular dimer fluorescent protein (IDFP)) (1) comprising a first
CC polypeptide peptide-bonded to a second polypeptide, where the first and
CC second polypeptides are found in nature as monomers of a multimeric
CC protein and the first and second polypeptides are not fluorescent donor
CC and acceptor to each other, and (1) is fluorescent when excited. (1) is
CC useful for monitoring the interaction of two polypeptides of interest
CC which involves contacting a first polypeptide and the second polypeptide.
CC (1) is also useful for screening for a compound that modulates the
CC interaction of first and second member of specific binding pair which
CC involves contacting a first polypeptide and a second polypeptide in the
CC presence and absence of candidate modulator. (1) can be used as reporter
CC genes to monitor the activity of promoter sequences to investigate the
CC cellular localisation of fusion proteins, to mark cellular proteins for
CC fluorescence activated cell sorting (FACS) analyses of cell population,
CC to monitor viral vector infection, to monitor transgene expression
CC in vivo or in culture, and to monitor protein:protein interactions both
CC in vivo and in vitro. (1) is suitable for applications that rely on
CC fluorescence resonance energy transfer (FRET). The present sequence
CC encodes humanised Renilla reniformis green fluorescent protein (GFP),
CC which is given in the exemplification of the present invention.
XX
SQ Sequence 720 BP: 156 A; 229 C; 219 G; 116 T; 0 Other;

QY 256 AAGATGAGTAAACAATATTGAAGACACTGTTTACAGAACTAATGTGTATAAGTA 315
DB 1 ATGCTGAGCAAGACGACCTGTAAGAACACCGCCTCGAGAGATCATGACCTTCAAGTGT 60
QY 316 AATCTGGAGGAATTTGTAACAACCAATGTTTACATGAGAGGCTTGGCGCAAGGAAT 375
DB 61 AACCTGGAGGCGCTGGTGAACCAACCAAGTGTTCACCATGAGAGGCTGGCGCAAGGCAAC 120
QY 376 ATTTTATTCGGCAATCAACTGTTTCAGATTGTTGTCACGAAGAGGCCCACTGCTTTT 435
DB 121 ATCTGTTTCGGCAACAGAGCTGTGAGATCCGGTACCAAGAGGCCCCCTGCTTC 180
QY 436 GCATTTGATATTTGTCACCAAGCTTTCAATATGAGAACCGCTTTCAGAAATATTCG 495
DB 181 GCCTTCACATTCCTGAGACCCGCTTCATACAGGCAACCGCATTCACCAAGTACCC 240
QY 496 AATGATATATCAGATTAATTTATACAAATCTTCCAGCAGAGATTATGTAGCAACA 555
DB 241 GAGGACATCAGGACCTTCTTCATCCAGAGCTTCCCGCGCTTCGTGACGAGCGCAC 300
QY 556 TTACGTTACGAGATCGCGACTTGTGAAATTCGTTCAAGATTAATTAATAGAAGAC 615
DB 301 CTGCGCTACGAGAGACGCGGCTGTGAGATCCGACAGACATCAACCTGATCGAGAG 360
QY 616 AAGTTGCTTACAGACTCGAATACAAAGTAGTAAGTCTCCCAATATGATGCTCCGTCATG 675
DB 361 ATGTTGCTGATCCGCTGAGGTACAAAGGCGGCAACTTCCCAAGCAAGCGCCCGTATG 420
QY 676 CAGAGACTATCTTGAATAGAGCCCTTCAATTGAAGCCATGACATGAATAATAGCGCTC 735
DB 421 AAGAAGACATCAACCGGCTGAGAGCCAGCTTTCAGAGTGTGTACATGAAGAGCGCTG 480
QY 736 TTGCTCGGCGAGTAATTTCTTGTATTAACCTAAGCTGCGGAATTAATTCATGTCAC 795
DB 481 CTGCTGGCGAGGTGATCTGCTGATCCGCTGACCGCTGACAGCGGCAAGTTCACACCTCCAC 540
QY 796 ATGAAACATTAATTAAGTGAAGTGAAGTGAAGAGAGTTCCTTCGATATCTTTTAT 855
DB 541 ATCCGCAACCTGATGAAGAGACAGGCGTGTGAGAGACTTCCCGACGATCCATTCATC 600
QY 856 CAACATCGTTTGGAAAGACTTACGTAGAAGAGCGGGGTTCTGTGAAGAGCATGAGACT 915
DB 601 CAGCACCCTCGTGAAGAACACTGACGTGAGAGAGCGGCGCTGTGAGAGCAGAGACC 660
QY 916 GCTATTGCTCAAAATGACATCTATAGAAAACCACTAGATCTTACACGAATGGTTTAA 975
DB 661 GCCATCGCCAGCTGACCAACCGCTGGCAGACCTGCACGATGGGTGTA 720
RESULT 14
AAD22204
ID AAD22204 standard; DNA: 873 BP.
XX
AC AAD22204:
XX
DT 12-FEB-2002 (first entry)
XX
DE Renilla reniformis green fluorescent protein encoding DNA, clone-3.
XX
KM Green fluorescent protein; GFP: bioluminescence generating system; toy:
KM luciferase; finger paint; slimy play material; fishing lure; sparkler;
KM doll; balloon; personal care item; cosmetic; bath powder; body cream;
KM tooth paste; mouth wash; soap; body paint; ornamental transgenic plant;
KM bubble bath; fountain; fairy dust; food; gelatin; icing; frosting; bear;
KM wine; champagne; milk; soft drink; ice cube; ice; foot bag; beverage;
KM dry ice; textile; clothing; paper product; greeting card; wrapping paper;
KM sea pansy; ds.
XX
OS Renilla reniformis.
XX
FH Key Location/Qualifiers
FT CDS 61..762

FT		/*tag=	a	/product= "Renilla reniformis green fluorescent protein"
FT				
PN	XX	WO200168824-A2.		
PD	XX	20-SEP-2001.		
PP	XX	15-MAR-2001; 2001WO-US08277.		
PR	XX	15-MAR-2000; 2000US-189691P.		
PA	XX	(PROL-) PROLUME LTD.		
PA	XX	(BRYA/) BRYAN B J.		
PI	XX	Bryan BJ, Szent-Gyorgyi C, Szczepaniak W;		
DR	XX	WPI: 2002-010561/O1.		
PT	XX	P-PsDB: AAEI3384.		
PT	XX	Nucleic acids encoding Renilla reniformis green fluorescent proteins,		
PS	XX	useful in diagnostic bioluminescence procedures -		
PS	XX	Claim 3a; Page 167-168; 175pp: English.		
CC	XX	The patent discloses sea pansy (Renilla reniformis) green fluorescent		
CC	XX	proteins (GFP) and their corresponding polynucleotides. The invention		
CC	XX	also relates to sequences of the bioluminescence generating system		
CC	XX	(e.g. luciferase). R. reniformis GFP are used in diagnostic methods		
CC	XX	and in the production of novelty items such as toys (e.g. squirt gun,		
CC	XX	pellet gun, toy "Halloween" eggs, toy cigarettes, board/card game		
CC	XX	toys), finger paints, slimy play material, bubbles in bubble making		
CC	XX	toys, fishing lures, dolls, sparklers, magic wand toys, balloons,		
CC	XX	personal care item (e.g. cosmetic, bath powders, body creams, tooth		
CC	XX	pastes, mouth wash, soaps, body paints, bubble bath) ornamental		
CC	XX	transgenic plants, fountain, fairy dust, food (gelatins, icings,		
CC	XX	frosting, beers, wine, champagne, milk, soft drinks, ice cubes, ice,		
CC	XX	dry ice, beverage), textile (foot bag, clothing) and/or paper product		
CC	XX	(greeting cards, wrapping paper). The present sequence is R. reniformis		
CC	XX	GFP clone-3 DNA.		
SO	XX	Sequence 873 BP; 295 A; 166 C; 180 G; 232 T; 0 other:		
		Query Match 22.0%; Score 237.8; DB 24; Length 873;		
		Best Local Similarity 56.9%; Pred. No. 2.2e-46;		
		Matches 456; Conservative 0; Mismatches 342; Indels 3; Gaps 1.		
OY	280 AACACTGGTTTCACGAAGTAATGTCTGAAGAATACTCGAAGCAATTGTAAACANC	339		
DB	73 AAACCTTGTTTACAGAACTGATGCCCTACTAAATCACTTAGAAGACTGGTGGCCAC	132		
OY	340 CATGTTTTTACAATGGAGGGTTGCGGCAAAAGGAATATTTTATCGGCANTCACTG	399		
DB	133 CACGCTTTCTCATGTGAAGAGACTTGGCGCAAGCAACATTTTGAAGAACTCAAGAG	192		
OY	400 CAGATTTCGTGCACAAAGGGCCGCACAGCCTTTGCAATTTGATATGTGTCACCAG	459		
DB	193 AAGATATCGGTAAACAAAAGCGCACACCTCCATTCGCATTTTGATATGCTATGTGG	252		
OY	460 TTTCATATGGCAACCGTACTTTCACGAATATTCGAATGAATATCAATATTTTATA	519		
DB	253 TTTTCATATGGCAACAGACTTATATCCGGTTACCCAGAAATTTCCGACTACTTC	312		
OY	520 CAATCATTTTCCAGCAGGATTTATGATGACAGAACATTCGTTACAGAGATGGCGACT	579		
DB	313 CAGTGTGTTCCGAAGGCGTTTACTTACGAGAAACATTCGTTATCAGATGGAGGACT	372		
OY	580 GTTGAATTCGTTTCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	639		
DB	373 GCATTTGTTAAATTCGATATTAAGCTTTGAAGAATGTTGAATTTATATAGTATGAC	432		
OY	640 AAAGTAGTAACCTCCAGATGATGCTCCCGCATGACAGAGAAGACTATCTTAAGAATA	699		
DB	433 AAAGCAAGGATCTACGTGCATGGGACCGACGATCATCTACCAAGAGACTCGTGGTAT	492		

OY	700	CCCTTCATTTGAAGCCATGTACATGATTAATGCGCGTCTTGCTGCGGGAAGTAATTTCTTGTG	759
Db	493	CCATCGTATGATGTCAAAGTACACCAATGTCTCAGTTATATAGGGAAATGTTAATATACGA	552
OY	760	TATTAACGTAACCTCTGGGAATTTATTAATGTCACATGAAACATTAATGAAGTCGAAA	819
Db	553	TTTCAACTTTCGAACGTGCGACAGCATTTTCACATTACACATGAGGACAGTTTACAAATCAAG	612
OY	820	GGTGTAGTAAAGAGTTCCTTCGTATCATTTTATTCACATCTGTTGGAAAAGACTTAC	879
Db	613	AAGCAGTGGGAACATATGACCTGTGTATCATTTTCATTCACACATCGGCTCTTAAAGACCAAT	672
OY	880	GTGAC---AGACGGGGGCTTCGTTGAAGACACATGACAGCTGATTTGGCTCAATGACATCT	936
Db	673	GTGGACACAGCCATGTTACGTTGTGGCAACAGACAGACATTTGCAGCGCATTTCTACA	732
OY	937	ATAGGAAACCCACTGAGATCCTTTACACAGCAATGGTTTAAACACAGTTCATTACTTTTTC	996
Db	723	ATCAAAAAAATVTGAAGGCTCTTTACCATGATACATGCTGACACAAATATATCTATGACGTA	792
OY	997	CAATTTCGTTTCATGTCAATAATATATTTTAAACAATTATCAATGTTTGTGATATG	1056
Db	793	GCATTTTTTTGGAAATPATTAAGTGTATGTTCAATAAATATTAAATATATATGCTTTTCA	852
OY	1057	TTTGTAAAAAATAAAAAA 1077	
Db	853	AAAAAAAAAAAAAAAAAAAA 873	
RESULT 15			
ID	AAD22203		
AC	AAD22203	standard: DNA: 860 BP.	
XX			
XX			
DT	12-FEB-2002	(first entry)	
XX			
DE	Renilla reniformis green fluorescent protein encoding DNA, clone-2.		
XX			
KM	Green fluorescent protein: GFP: bioluminescence generating system: toy;		
KM	luciferase; finger paint; slimy play material; fishing lure; sparkler;		
KM	doll; balloon; personal care item: cosmetic; bath powder; body cream;		
KM	bubble bath; mouth wash; soap; body paint; ornamental transgenic plant;		
KM	tooth bath; fountain; fairy dust; food; gelatin; icing; frosting; beer;		
KM	wine; champagne; milk; soft drink; ice cube; ice; foot bag; beverage;		
KW	dye; ice; textile; clothing; paper product; greeting card; wrapping paper;		
KW	sea pansy; ds.		
XX			
OS	Renilla reniformis.		
XX			
PH	Key	Location/Qualifiers	
FT	CDS	57..758	
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FT		/product= "Renilla reniformis green fluorescent protein"	
XX			
PN	WO200168824-A2.		
XX			
PD	20-SEP-2001.		
XX			
PE	15-MAR-2001; 2001WO-US08277.		
XX			
PR	15-MAR-2000; 2000US-189691P.		
XX			
PA	(PROL-) PROLUME LTD.		
XX			
PA	(BRYA-) BRYAN B J.		
XX			
PI	Bryan BJ, Szent-Gyorgyi C, Szczepaniak W;		
XX			
DR	WI: 2002-010561/01.		
XX			
DR	P-PSDB: AAEI3384.		
XX			
PT	Nucleic acids encoding Renilla reniformis green fluorescent proteins,		

PT useful in diagnostic bioluminescence procedures -
XX
XX Claim 3a: Page 165-167; 175pp; English.
XX
CC The patent discloses sea pansy (Renilla reniformis) green fluorescent
CC proteins (GFP) and their corresponding polynucleotides. The invention
CC also relates to sequences of the bioluminescence generating system
CC (e.g. luciferase). R. reniformis GFP are used in diagnostic methods
CC and in the production of novelty items such as toys (e.g. squirt gun,
CC pellet gun, toy "Halloween" eggs, toy cigarettes, board/card game
CC toys), finger paints, slimy play material, bubbles in bubble making
CC toys, fishing lures, dolls, sparklers, magic wand toys, balloons,
CC personal care item (e.g. cosmetic, bath powders, body creams, tooth
CC pastes, mouth wash, soaps, body paints, bubble bath), ornamental
CC transgenic plants, fountain, fairy dust, food (gelatins, icings,
CC frosting, beers, wine, champagne, milk, soft drinks, ice cubes, ice,
CC dry ice, beverage), textile (foot bag, clothing) and/or paper product
CC (greeting cards, wrapping paper). The present sequence is R. reniformis
CC GFP clone-2 DNA.
XX
SO Sequence 860 BP; 298 A; 162 C; 175 G; 225 T; 0 other:

Query Match 21.2% Score 229; DB 24; Length 860;
Best Local Similarity 57.3%; Pred. No. 2.5e-44;
Matches 454; Conservative 0; Mismatches 335; Indels 4; Gaps 2;

QY 280 AACACTGTTTACAGAGAGTAATGCTGATAAAGTAATCTGAGAGCAATTTGAACAC 339
DB 69 AACTGTTGTTGAAGAGAGTATGCTTACTAAATCACTAGAGAGACTGTTGCGCAG 128
QY 340 CATGTTTTTACATGAGAGGTTGCGCAAGGAAATATTTTATTCGCAATCAACGTGT 399
DB 125 CAGCGTTTTCATGAGAGAGTGGCGAAGCAACATATTGAGAGCACTCAAGAGGTG 188
QY 400 CAGATTGCTGTCAGAAAGGCGCCAGTCCCTTTTGCATTGATATTTGTCAGCAGCT 459
DB 185 AAGATATCGGTACAAAGGCGCCAGCTCCATTCGATTGATATGTAATCTGTATCTGT 248
QY 460 TTTCATATTCGCAACCGTACTTTCAGCAATATCCGAATGATATATCAGATTAATTTATA 519
DB 249 TTCTCATATGGAACAGACCTTATACGTGTTACCCAGAAAGAAATTTCCGACTTTCCTC 308
QY 520 CAATCATTTCCAGCAGGATTATGTATGAAAGCAATTCAGTACGAGATGGCGGCTT 579
DB 309 CACTCGTTTCAGAGAGCTTTACTTACGAGAGAAACATTCGTTATCAGATGAGAGACT 368
QY 580 GTTGAATTCGTTACAGATATAATTTAATAGAGACAGTTCCGTTACAGAGTCGAATAC 639
DB 369 GCATTTGTTAATCTGATTTAGCTTGAAGATGTAATTCAATGATGTAAGACTTC 428
QY 640 AAGGTAGTAACCTCCAGATGATGCTCCGCTATGACAGAGACTATCTTAGAATAGAG 699
DB 429 AAGCGAGAGATCTACCTCCAGTGGAGCAGTATCCAGCAGACATCGTGGGTATCCAG 488
QY 700 CTTTCATTTGAACCGCATGTACATGATTAATGGCGTCTTGSTGCGGAGTAATTTCTGTG 759
DB 489 CCATCGTATGAGTCAATGATACCAATGTCACCTTCACTTATAGGGATGTATTAATAGCA 548
QY 760 TATTAACCTAACTCTGGAATATTTATTCATGTCAGATGAACATTAATGAAGTCGAAA 819
DB 549 TTCAACTTCAAAGCTGGCAAACTTTACCTTACACATGAGACGTTTACAAATCAAG 608
QY 820 GGTGTAGTAAGGAGTTCTTGATCATTTTATTCACATCGTTTGAAGAAAGACTTAC 879
DB 609 AAGCCAGTGAAGAACTATGCCATTTGATCATTTTCATCCAGCATCGCTGTTAAGACCAAT 668
QY 880 GTAGA--AGACGGGGGCTGTTGAACAGAGAGCTGCTATGCTCAATGACATCT 936
DB 659 GTGGACAGACCGCTGTTAGCTTTGTCAGACAGAGACAGCAATTTGACGGCAATCTACA 728
QY 937 ATAGGAAGACCACTAGATCTTACAGGAATGGTTAAACAGACTTACATTTACTTTTC 996
DB 729 ATCAAAAAAATTGAAGCGTCTTTAG-CATAGATATCTATACACAAATTAATTTGATGACGT 787

QY 997 CAATTCGTTTTCATGTCGAATAATATATTTTAAACATTAATCAATGTTTGTGATATG 1056
DB 788 AGCATTTTGGAAATATATAGTGTATTTGTCATTAATAATTAATTAATTAATTAATTA 847
QY 1057 TTTGTAAAAAAA 1065
DB 848 AAAAAAAAAAAAA 860

Search completed: January 16, 2003, 12:19:52
Job time : 272.494 secs

ECORI digestion of *Drosophila* DNA provided by the BGP from the isogenic strain y2; cn bw sp, the same strain used for the BGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

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  /dp_xref="taxon:7227"
  /clone="BACROBK10"
  /clone_1lb="RPCL198"
  /note="end : TET3"
  64 c 131 g 202 t 503 others
BASE COUNT
ORIGIN
201 a

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Query Match	5.4%	Score 58.4;	DB 17;	Length 1101;
Best Local Similarity	17.3%	Pred. No. 0.14;		
Matches 101;	Conservative 245;	Mismatches 236;	Indels 2;	Gaps 1

QY	496	AATATATATGACATTAATTTTATACATCATTTCCGACGAGTTATGATGAAGACA	555
Db	985	DADGAGRDGGRRKOKKDRKDSDDDKKGGKKKAAKAAKAAATKWMDDMDKDKMKDGA	926
QY	556	TTACGTTACGAGATGGCGGCACTTGTGAATTCGTCGAGATATAATTTATAGAAAC	615
Db	925	KDRKADDDDGAGCKDDGKG - KDADDPTDGTKDDDKDKMDMKAKGTMGDATWMAA	868
QY	616	AAGTTCGTCTACAGAGTCGCAATCAAAAGTACTAATTCGCCGATGATGTCGCCGTATG	675
Db	867	TDWMMWMAADWWTYDAAADWMAADRDMDAMKMDAMAGCAFTARDRWGBAGKRG	808
QY	676	CAGAGACTATCTAGGAATAGAGCCCTCATTTTGAAGACCATACGATATAATGGCTC	735
Db	807	GAKRRRBRKADDRDAADRDRAATWTWTWTTTTRDDTDWKKKIDTTRAAADRTDRO	748
QY	736	TTGGTCGGCGAAGTAATTTCTGTCTATAACTAACTCGGGAATATTAATTCATGTCAC	795
Db	747	DDDRDRAGTAGAKRRWRTWKRWRKRDTRMDADADDTARDDRBRDGDGAGCKKGTG	688
QY	796	ATGAAAACTTAATGAAGTCGAAAAGTGTAGTAAGAAGATTCCTTCGTATCATTTATT	855
Db	687	RKRRRRRATWDRIDWMAADAAWTTTDDTDWPKRDRRRRGAARRRRTRARAAMDWT	628
QY	856	CAACATCGTTTGGAAAAGACTACCTAGAGAGCGGGGGTTCGTGACAGCATGAGACT	915
Db	627	WKAMDAMKMKWKTIRADWDMDWAADPTDARKKDRDMAKRAARARDRARADRRWTT	568
QY	916	GCTATTCGCTCAATGACATCTATAGAAAACACACTAGATCCCTTACAGAAATGGTTAA	975
Db	567	KGKTTTATWTTWARAAMWMMWMAATTTATWTTTWTWTWTTTTTTTTTTTTAAWMA	508
QY	976	ACACAGTTACATTACTTTTCCATTCGATTCGTTTCATGTCACAAATAATTTTAAACAA	1035
Db	507	AMWTATWAAATTAAMAAAAAAMAATTTTTTTTTTTTWTWAMTAAAWMTAWTWTWT	448
QY	1036	TTATCATGTTTGTGATATGTTTGTAAAAAAMAAAAAAMAAAAA 1079	
Db	447	WMAATTTTTTWTWMAATTAATTTTWTWTAAMAAAAAAMWMM 404	

RESULT 2	LOCUS	DEFINITION
CNS0006J	1101 bp	DNA
CNS0006J		linear
		GSS 03-JUN-1999
		Drosophila melanogaster genome survey sequence TEF3 end of BAC #
		BACR01M22 of RPCR-98 library from Drosophila melanogaster (fruit
		fly), genomic survey sequence.

ACCESSION	AL062049
VERSION	AL062049.1
KEYWORDS	GT:4938511
SOURCE	GSS.
ORGANISM	Drosophila melanogaster.
	Drosophila melanogaster
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Séquençage :
JOURNAL

COMMENT

collaboration with the Berkeley Drosophila genome project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org>. The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammosser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

```

source
1. .livi
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR01M22"

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Best Local Similarity	27.2%	Pred. No. 0.37:			
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QY	81	TAATCGAACCCACACAACAACCTCTTAAATAAGCCGCACTTTACATATATCTAAGAGAGCC	140		
Db	516	TAMTGTGAAAAAAMAAAMWTTTAAAGAAAAAAMAAAMATATKAAATTTTTTTRRRTRAGT	575		
QY	141	CTCATTTAAGAGTACTATAAATATATATATGATGATGACTATAGCACTCCGCTTAGACA	200		
Db	576	ATTTRDTTAKAAAAAATAATATTAGAAABGAAAAAARAAAGCTTTGGAAGAAA	635		
QY	201	GACAGTGTGCACAGAGTACTCTTGTTAATGCAATCGAAAGCGTCAAGAGAGATAGAT	260		
Db	636	AAAAAANAATATAAKKAAKAAAGGAAAAAATAAATAAKAAKMRIGTGTATAAAAAA	695		
QY	261	GAGTAAACAATATTGAACAACACTTTGTTTACAGAGACTAATGTCGTATAAGTAAATCT	320		
Db	696	AAAAAAGAGGAKKGGGKACARARAGRGGRRAAARAATAKTRKTKTKTKRRRAAGRA	755		
QY	321	GGAAGAGATTGTAACCAACCACTGTTTGTACAAATGAGAGGTGGCGGCAAGAGATATTTT	380		
Db	756	RRAMGAAAAAARAAADAAATKTGTGTTAKKAAAMRTAAKKDKMKTATPAAAAKAAARTRDMTT	815		
QY	381	ATTGGCAATCACTGCTTCAGATTCGTGTCAAGAACGAGGGCCCACTGCCTTTTGCAATT	440		
Db	816	AKAKDKTKWCAAAAAATGAGAGAAAGRRMRGRKDKDTRRARAGACDGDADAKAAAMMAAAM	875		
QY	441	TGATTTGTGTGACAGCTTTTTCATTTATGCGAACGCTACTTTCAGCAAAATATCCGAATGA	500		
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QY	501	TATATCAAGATTATTTTATACAATCAATCTTTCAGACAGATTTTATGTATGAAGCAACTTACG	560		
Db	936	RCARAGAAKAKRRRAKDDAKDKWKKWDIDAAMAAKAKGTDGMRKRRRAKTKGMRARAKD	995		
QY	561	TTACGANAAGTGGGCACTTTGTTGAATTCGTTCAATATTAATTTAATGAAGACAAGTT	620		
Db	996	RKRAAADDTTMRGTATKMMWTTDKDTRKAAKGGKAAKTTTTRTDRAKAAKAKDPT	1055		

QY	621	CGCTACAGAGTCGAATCAAAAGAGTAA	649
Db	1056	AATRTATATKWDADKAKADAKAKWGADA	1084
LOCUS	CNS0106X	1101 bp	DNA
DEFINITION	Drosophila melanogaster genome survey sequence 77 end of BAC BACN03K20 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.		
ACCESSION	AL098595		
VERSION	AL098595.1	GI:5610206	
KEYWORDS	GI:5610206		
SOURCE	Drosophila melanogaster.		
ORGANISM	Drosophila melanogaster		
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
AUTHORS	1 (bases 1 to 1101)		
TITLE	Genoscope.		
JOURNAL	Direct Submission		
COMMENT	Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage; BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)		
FEATURES	Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billard at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.		
source	Location/Qualifiers		
	1..1101		
	/organism="Drosophila melanogaster"		
	/db_xref="taxon:7227"		
	/clone="BACN03K20"		
	/clone_11b="DrosBAC"		
	/plasmid="pBelobAC11"		
	/note="end : 77"		
BASE COUNT	258 a 107 c 60 g 175 t 501 others		
ORIGIN			
Query Match	4.9% Score 53; DB 17; Length 1101;		
Best Local Similarity	20.4% Pred. No. 1.5;		
Matches	82: Conservative 154; Mismatches 165; Indels 0; Gaps 0;		
QY	679	AAGACTATCTTAGCAAGTACAGCCCTTCATTTGACGCGATCATGATATAGCGCTTTG	738
Db	620	ATGCTATATRTAAATCTAKTADTADTGTAAATATATKATKRAKKADPAKWDKDKATK	679
QY	739	GTCGGCGAAGTAAATCTTCGTATACCTTAACCTTGGCAAAATATTATTCATGTCACATG	758
Db	680	AKAKKKAARAKAKAAKATATGKDAKAKAKAKAKATKRAKAAATATATTAADAADK	739
QY	799	AAAACATTATGAAGTCGAAGCGTGTACTAAAGAGAGTTCCCTTCATATCTTATTTAA	858
Db	740	GAKDKAKAKAADADADKRRMDAKKRRKRAKAKAKAAADADADADKADKADAKADAA	799
QY	859	CATCTTTGGAAGAACCTACCTAGACAGCGGGGCTTCGTTGAACAGACATGACACTGCT	918
Db	800	DADDDGCGDKKRAKDKKKKKKDKKAMDKKKAKKAAAKADAAADAKARRRADDK	859
QY	915	ATTGCTCAATGATGCTATAGGAAACACCTAGATGCTTACACGATGGGTTAAACA	978
Db	860	DKAKADAAKAKAKKDDDDKAAATKAKAKATKAKDKAKAKKKKKKKDKAKAKAKADA	919
QY	979	CAGTTACATTCCTTTTTCGCAATTCGCTGTTTCATGCAATATATAATTTTTTAAACATTA	1038
Db	920	KDKDDKDDDDKDKKAKKADKRRKKKDKRDKAKKDDDKDKAKDDKDKKADAKAKAA	979
QY	1039	TCAATGTTTGTGATATGTTGTGTAATAAAAAAAAAAAAAAAAAAAAAA	1079

Db	980	KADADAKAKAKAKAADDPAADAKAKAADDPAADAKAKAKAKAD	1020
RESULT 4			
LOCUS	AL534260/c	865 bp	linear
DEFINITION	AL534260 LTI-FL013_FBrn1	Human sapiens cDNA clone CS0DF005YP20 5	EST 13-FEB-2001
ACCESSION	AL534260		
VERSION	AL534260.1	GI:12797753	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.		
AUTHORS	Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - France Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.		
FEATURES			
source	1. 865 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="CS0DF005YP20" /clone_lib="LTI-FL013_FBrn1" /dev_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)" /lab_host="DH10B" /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a Molt-Oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@life.com URL : http://fulllength.invitrogen.com"		
BASE COUNT	144 a 197 c 107 g 321 t	96 others	
ORIGIN			
Query Match	4.7%.	Score 51:	DB 9: Length 865;
Best Local Similarity	40.4%.	Pred. No. 3.9;	
Matches 105:	Conservative 22:	Mismatches 133:	Indels 0: Gaps 0:
0y	97 AACCTCTAAATAATGACCACTTTCATATATATCATAGACAGCGCTCTTAAAGAGTACT	156	
Db	420 AAAAATAATGAAAAAATAATTTTANGRNAATAARAATAATGAAAAAARCAATGARAG	361	
0y	157 AAAAATATATATATATAGATAGATATACAACCTCTGCGCTTAGACAGACAGTGTGCACAG	216	
Db	360 AAAAGARMAAAAGGAAAAARGTATAMARAAAAAARARAWGGAAGAGAAAAAANNNA	301	
0y	217 GTAACCTCTTGTATATGCAATGCAGAAAGCTCAAGACAGATTAAGATGATAGTAACAATATTG	276	
Db	300 AAANNNNNNNANNGTARMAAAARARARARAGAAAAARAAANNNNNNAAAAANNNG	241	
0y	277 AAGACACTCTGTTCACAGAGAGTATGTCGATATTAAGTAATCTGGAAGAAATTTGTAAC	336	
Db	240 NAGANNAAGGTGGCGAAGARAAAWGTTAATAAAARMAAAATATMARAATTTGGA	181	
0y	337 AACCATGTTTTTACAAATGA	356	
Db	180 GAATGTTGAAAAAATGAA	161	

LOCUS	Drosophila melanogaster genome survey sequence S6 end of BAC
DEFINITION	BACN12P22 of DrosBac library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	AL104456
VERSION	ALI04456.1 GI:5616067
KEYWORDS	GSS.
SOURCE	Drosophila melanogaster.
ORGANISM	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE	1 (bases 1 to 987)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage ; BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT	Determination of this BAC-end sequence was carried out as part of a collaboration with The European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk/. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaut at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelOBAC11.
FEATURES	Location/Qualifiers
source	1..987 /organism="Drosophila melanogaster" /db_xref="taxon:7227" /clone="BACN12P22" /clone_1lb="DrosBAC" /plasmid="pBelOBAC11" /note="end : Sp6"
BASE COUNT	257 a 122 c 122 g 241 t 245 others
ORIGIN	
Query Match	4.7%, Score 51; DB 17; Length 987;
Best Local Similarity	28.7%; Pred. No. 3.7;
Matches 114; Conservative	90; Mismatches 193; Indels 0; Gaps 0;
OY	683 CTATCTAGGAAATAAGCGCTCATTTGAGCCCATGTACATGAATAATGGCGTTCGCG 742
Db	546 MTAGWTDTRTGRTGRKKGRDKDMTTAGAAMAAADRAARDRRRRRBRKBNKKKKKKKT 605
OY	743 GCGAAGTAATTCTTGCTATAAACAATCCTGGGAATATATATTCATGCATCAATGAAA 802
Db	606 KTTTTTTTTTKAVMWCITBKCCCCCCCCCMMAAMMAAMMAAMMAAMMAAMMAAATTA 665
OY	803 CATTAATGCAAGTCGAAGGTGTAGTAAGAGATTCCCTTCATCATTTTATCAACATC 862
Db	666 TAAAAAAMMAAAAAAAAAAAATAATATAMMANNTNMWTMMWMWMTTTTTTTTTTAAW 725
OY	863 GTTTCGAAAAGACTTAGCAAGCGGGGGTTCGTTGAACAGCATAGACTGCTATTG 922
Db	726 AAAAAMMAAMMAAMMAAMWTTAWMATWMTTTTAAGAAATATTATTAATTMAAATTTTMMWTT 785
OY	923 CTCAAATGACATCTCTAGGAACAACCACTAGATGTCCTTACAGCAATGGGTTTAACACAGT 982
Db	786 ATTAATTAAMTAATTTWATTWATTTATTTAAATTAATTAATTAANKKWTTWTTTTTTTTT 845
OY	983 TACATTTACTTTTCCATTCGTTGTTTCATGTCGAATTAATATTTTAAACATTTATCAA 1042
Db	846 WMTATTAATTTTMMWMAAATAATMGSRMTMWMAATTAATAAAWATMAAANAAMWMDAA 905
OY	1043 TGTTTTGATATGTTTGTAAAAAAMMAAAMMAA 1079
Db	906 AWDMMWMAWMTAAAMWTTAAAAAAMMAAAMMAA 942
RESULT 6	
C90654	C90654 579 bp mRNA linear EST 20-Apr-1998
LOCUS	C90654 579 bp mRNA linear EST 20-Apr-1998

[illegible]


```
/plasmid="pBelobAC11"
/Note="end : 17"
BASE COUNT      298 a      172 c      106 g      316 t      312 others
ORIGIN
Query Match      4.4%; Score 48; DB 17; Length 1204;
Best Local Similarity 20.7%; Pred. No. 13;
Matches 94; Conservative 157; Mismatches 204; Indels 0; Gaps 0;

QY 115 ACATTACATTAATATCTAGACAGCGCCCTCATTTAAGATAGTAAATATATATATGAT 174
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1200 ADKKAATAATAWAAWAAKATATAKAWKAKAWKAAAAAATAAAAAAATAAADA 1141
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 175 AGAGTATACACTCTGCGCTTACAGACAGACAGTGTGCAAGAGTACGCTTTGTAATGCA 234
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1140 AAKKKAATAAATAADADAADAAAAAATAKAKAKAAAAAATAAAMKKAATAAATA 1081
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 235 ATCGAAAGCGTCAGAGATAGATAGCTAAACAATAATTGAAGAACAAGCTTTTACAA 294
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1080 AAKWKAATKDDDDKRAADAKKKKAKADADKADKDKKAKADAMDDADDAKKKK 1021
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 295 GAAGTATATGCTCGATTAATATCTGGAAGGATTTGTAACAACATGTTTACAAAG 354
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1020 KAKKKKKKKDDATDADWAAKAAKKKKKKKKKKKKKKAKAKAKKKKKKKKKKK 961
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 355 GAGGCTTGGCGCAAGATATTTTATTCGCAATCACTGCTGTCAGATTGTCACAG 414
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 960 KKKKKKKKKKAAKAAKAAAAAATAKAKKKKKKKKKKKKKKKKKKKKKKKKK 901
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 415 AAAGGGGCCCCACTGCGCTTTGCAATTTGATTTGTCACACGCTTTTCAATATGCAAC 474
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 900 AADKKAATAKAAKAAKKKKKDAADAKKKKKKKKKKKKKAAKADDAKKKKKKAG 841
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 475 CGTACTTTCACGAATAATCGAATGATATCATGATTTTATACATCATTTCCAGCA 534
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 840 AAAAAKKKKGGGGGGGAGGAGGAAAGATTTTAKTTDTTKTAKADAKTTTKTTTWA 781
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 535 GGATTTATGTATGAACGAAACATTACCTTACGAAGA 569
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 780 TKAGAKWAKTKTRAAKDARGKDAATTKAARAAGA 746
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
CNS00DKY      928 bp      DNA      linear      GSS 04-JUN-1999
LOCUS
DEFINITION   Drosophila melanogaster genome survey sequence T7 end of BAC #
BAC27A24 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION   AL071865.1 GI:4948170
VERSION
KEYWORDS
SOURCE      GSS.
ORGANISM    Drosophila melanogaster.
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE    1 (bases 1 to 928)
AUTHORS
TITLE
JOURNAL
COMMENT      Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr)
            - Web : www.genoscope.cns.fr)
            Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mamoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
```

p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

```
FEATURES
    source
        1..928
            /organism="Drosophila melanogaster"
            /db_xref="Caxon:7227"
            /clone="BAC27A24"
            /clone_lib="RPCI-98"
            /note="end : 17"

BASE COUNT      262 a      70 c      84 g      321 t      191 others
ORIGIN
Query Match      4.4%; Score 47.6; DB 17; Length 928;
Best Local Similarity 32.0%; Pred. No. 17;
Matches 105; Conservative 62; Mismatches 161; Indels 0; Gaps 0;

QY 752 TTCTGTCTATAACTTAACCTGCGCAATATTATTCATGTCACATGAACATTAAATGA 811
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 479 WTATATTATATATAATATATATGATGATTAATTTTATKAWMAAATAATTTTWT 538
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 812 AGTCGAAGGCTGATGAAGAGCTTCCTGATCATTTTATTCACATCGTTGGAAA 871
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 539 WTTTTWMAAAMTATTTTWTTTTWTWTTTAAATTTTAAATTTTAAATTTTAA 598
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 872 AGACTTACGTAGAGAGCGGGGCTGTCGACGACATGAGACTGCTATTCGCAATGA 931
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 599 AWKATTTTATATWATATWMAATATWATATATATATTTTWTATTTTATATTA 658
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 932 CATCTATAGAAAACCATAGATCCCTTACAGCAATGGGTTTAAACAGTATACATTA 991
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 659 AAWMAAATAAATAAATAAATAATTTTAAWATAAATAAATAATTTTATTTT 718
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 992 TTTTCAATTCGCTGTCATGCAATATATTTTAAACATTTATCAATGTTTGG 1051
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 719 TTTTATTTWATAATAAATAATWMAATWTDKNNNNNAWMAWMAWMAWMAWMA 778
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1052 ATATGTTGTAAATAAATAAATAAATAA 1079
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 779 WWWWWWWMAAATAAATAAATAAATAA 806
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
CNS0161H/c     1201 bp      DNA      linear      GSS 26-JUL-1999
LOCUS
DEFINITION   Drosophila melanogaster genome survey sequence T7 end of BAC
BACN15018 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION   AL106175.1 GI:5620521
VERSION
KEYWORDS
SOURCE      GSS.
ORGANISM    Drosophila melanogaster.
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE    1 (bases 1 to 1201)
AUTHORS
TITLE
JOURNAL
COMMENT      Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billand at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBelobAC11.

FEATURES
    source
        1..1201
            Location/Qualifiers
```

```
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_1ib="BACN15018"
/clone_1ib="DrosBAC"
/p1asmid="pbelioBAC11"
/notes="end : 17"

BASE COUNT      120 a      163 c      157 g      513 t      248 others
ORIGIN

Query Match      4.4%: Score 47.4; DB 17; Length 1201;
Best Local Similarity 39.7%: Pred. No. 16;
Matches 102; Conservative 32; Mismatches 123; Indels 0; Gaps 0;

OY      82  ATTCGAACCCACCAACCTTAATAATAGCCACATTTACATATATCTAAGACGCC 141
DB      414  AAAAAAAAAAAAAAAAAAATACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAT 355
OY      142  TCATTAGAGTGTAGTAAATATATATATGATAGAGTATACAACTCTGCCTTAGACAG 201
DB      354  ACATTAATAAAAAAAAAACCAATATATATATATARAAMAAACAAAMMANATGTGMAAAA 295
OY      202  ACAGTGTCAACAGACTACTCTTTTAAATGCAATCCAAACCGTCAAGAGATTAAGATG 261
DB      294  TAAAAAAMAMMAAAMAAACAAAMMAAAMAAARAAAMAAACMTAAMAMAAATAAAAAM 235
OY      262  ACTAACAACATATTTGAGAACACTGTTTACAGAGAGTATGCTATTAAGTAAATCTG 321
DB      234  AAMACCAAAAAAAAAAAAAAAAAAMTCRAAAAMTAAAMAAAMAAAMAAARAAACAAATGCR 175
OY      322  GAAGGATTTGTAACCAA 338
DB      174  RMAAAAAAAAAAAAAAM 158

RESULT 12
CNS00FMC      1101 bp      DNA      linear      GSS 03-JUN-1999
LOCUS      Drosophila melanogaster genome survey sequence TET3 end of BAC:
DEFINITION      BACR31N17 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION      AL070972.1 GI:4550813
VERSION      AL070972.1
KEYWORDS      GSS.
SOURCE      Drosophila melanogaster.
ORGANISM      Drosophila melanogaster.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
Genoscope.
REFERENCE      Direct Submission
AUTHORS      Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
TITLE      BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
JOURNAL      - Web : www.genoscope.cns.fr)
COMMENT      Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
location/Qualifiers
1. .1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
```

```
/clone="BACR31N17"
/clone_1ib="RPCI-98"
/notes="end : TET3"

BASE COUNT      390 a      76 c      59 g      302 t      274 others
ORIGIN

Query Match      4.4%: Score 47.2; DB 17; Length 1101;
Best Local Similarity 43.4%: Pred. No. 18;
Matches 69; Conservative 27; Mismatches 63; Indels 0; Gaps 0;

OY      920  TTGCTCAATGACATCTATAGAAACCACTAGATCTTACAGAGTGGTTAAACAC 979
DB      846  TTATTAATAAAMATATATATATATATAABAAAMWTAAMATTMANATATATAMTAT 905
OY      980  AGTTACATTAAGTTTTCGAATTCGTTTCATGTCAAATAATATTTTAAACAATTAT 1039
DB      906  ATTMAATATATTTTATTAATAATATATATATATATATATATATATATATATATAT 965
OY      1040  CAATGTTTGTGATATGTTGTAATAAAAAAAAAAAAAAAAAA 1078
DB      966  TATTTTATTTTATTAATAAATAAATAAAMAAAMAA 1004

RESULT 13
CNS00H2T/C      442 bp      DNA      linear      GSS 03-JUN-1999
LOCUS      Drosophila melanogaster genome survey sequence TET3 end of BAC:
DEFINITION      BACR35M12 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION      AL074554.1 GI:4953930
VERSION      AL074554
KEYWORDS      GSS.
SOURCE      Drosophila melanogaster.
ORGANISM      Drosophila melanogaster.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 442)
Genoscope.
REFERENCE      Direct Submission
AUTHORS      Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
TITLE      BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
JOURNAL      - Web : www.genoscope.cns.fr)
COMMENT      Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
location/Qualifiers
1. .442
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"

FEATURES
source
BASE COUNT      71 a      13 c      18 g      302 t      38 others
ORIGIN

Query Match      4.4%: Score 47; DB 17; Length 442;
Best Local Similarity 43.8%: Pred. No. 28;
Matches 113; Conservative 17; Mismatches 128; Indels 0; Gaps 0;

OY      81  TATTCGAACCAACCAACTTAAATAACCCACATTTACATATATCTAAGACGCC 140
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[illegible]

RESULT 14	CNS00DKY/c	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
	CNS00DKY	928 bp	DNA	linear	GSS	04-JUN-1999							
	Drosophila melanogaster genome survey sequence T7 end of BAC #												
	BACR2A24 of RPc1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.												
	AF071865												
	AF071865.1	GI:4948170											
	GSS												
	Drosophila melanogaster.												
	Drosophila melanogaster												
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.												
	1 (bases 1 to 928)												
	Genoscope.												
	Direct Submission												
	Submitted (02-JUN-1999)	Genoscope	:	Centre National de Sequencage	:								
	BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr												
	- Web : www.genoscope.cns.fr												
	Determination of this BAC-end sequence was carried out as part of a												

melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammocer in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCL-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2: cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at <http://bacpac.med.buffalo.edu/drosophila-bac.htm>.

FEATURES	
source	
1..928	Location/Qualifiers
/organism="Drosophila	melanogaster"
/db_xref="taxon:7227"	
/clone="BACR27A24"	
/clone_11b="RPCL-98"	
/note="end : 17"	
262 a	70 c 84 g 321 t 191 others
BASE COUNT	
ORIGIN	

	Query Match	4.3%	Score 46.8:	DB 17:	Length 928:
	Best Local Similarity	26.6%:	Pred. No. 23:		
	Matches	41:	Conservative	63:	Mismatches 50:
					Indels 0:
					Gaps 0:
OY	926	AATGACATCTTATAGCAAAACCACTTAGGCCTCTTACACAAGATGGCTTTAATACACAGTTAC	985		
Db	866	AAAAAAATTTCTAAADAMAAAMKISCVIMIRIKIMIRIKIMIRITMIRINNNNNNNNNNTTTT	807		

Oy	986	ATCTCTTTTCCAACTCGCTTCATGCACTCAATATATTTTAAACATATACAACT	1045
		: : : : : : : : : : : : : : : : : :	
Db	806	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	747
Oy	1046	TTTGTGATATGTTGTTAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1079
		: : : : : : : :	
Db	746	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	713
		: : : : : : : : :	

RESULT 15	
CNS001FB/c	
LOCUS	1101 bp DNA linear GSS 03-JUN-1999
DEFINITION	CNS001FB Drosophila melanogaster genome survey sequence TET3 end of BAC # BAR04A23 of RPCT-96 library from Drosophila melanogaster [fruit fly], genomic survey sequence.
ACCESSION	AL060732
VERSION	AL060732.1 GI:4939397
KEYWORDS	GSS.
SOURCE	Drosophila melanogaster. Drosophila melanogaster
ORGANISM	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. I (bases 1 to 1101) Genoscope. Direct Submission Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	

COMMENT	FEATURES	SOURCE
<p>Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org/TheBDGP/Drosophila_melanogaster_BAC_library was prepared by Kazuhiro Oseegawa and Aaron Mamosser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPK1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.</p>	<p>Location/Qualifiers</p>	<p>1..1101</p>

FEATURES	location/Qualifiers
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	/organism="Drosophila melanogaster"
	/db_xref="taxon:7227"
	/clone="BACR04A23"
	/clone_lib="RPC1-98"
	/note="end : TEF3"
BASE COUNT	288 a 110 c 103 g 491 t 109 others
ORIGIN	
Query Match	4.3% Score 46.2; DB 17; Length 1101;
Best Local Similarity	38.7%; Pred. No. 28;
Matches 108; Conservative	32; Mismatches 139; Indels 0; Gaps 0;

[illegible]

Thu Jan 16 15:55:48 2003

us-09-710-058a-1.rst

Page 9

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Oy      344  TTTTACATGCAGGCTGCGGCAAGGCAATATTAT 382
      :| | : | :| | :| | |
Db      852  WTATAAATTAAAAATWTNTWAMWMAAAAATWTTTTT 814
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Search completed: January 16, 2003, 14:59:50
Job time : 1800.43 secs


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181 TACAACCTCGCCCTTAGACAGACAGTGTGCACACAGAGTAACCTCTGTTAATGCAATCGAA 240
181 TACAACCTCGCCCTTAGACAGACAGTGTGCACACAGAGTAACCTCTGTTAATGCAATCGAA 240
241 AGCGTCAAGAGATATAGATGAGTAAACAATATTGAAGAACCTTGTTTACAGAAGTA 300
241 AGCGTCAAGAGATATAGATGAGTAAACAATATTGAAGAACCTTGTTTACAGAAGTA 300
301 ATGTGCTATAAAGTAATTCGGAAGAAATGTATAACACCATGTTTTCATATGAGAGGT 360
301 ATGTGCTATAAAGTAATTCGGAAGAAATGTATAACACCATGTTTTCATATGAGAGGT 360
361 TCGGCAAAAGGGAATATTTTATTCGGCAATCAACCTGTTTCAGATTCGTACAGAAAGG 420
361 TCGGCAAAAGGGAATATTTTATTCGGCAATCAACCTGTTTCAGATTCGTACAGAAAGG 420
421 GCCCCACTGCTTTTGCATTTGATTTGTGTACACGCTTTTCAATATGGAACCGTACT 480
421 GCCCCACTGCTTTTGCATTTGATTTGTGTACACGCTTTTCAATATGGAACCGTACT 480
481 TTCACGAATATCCGAATGATATATCAGATTTATTTATCAATCATTTCCAGCAGGATTT 540
481 TTCACGAATATCCGAATGATATATCAGATTTATTTATCAATCATTTCCAGCAGGATTT 540
541 ATGTATGAACGAACATTAAGTACGAGATGGCGGACTTGTGAAATTCGTTCAGATATA 600
541 ATGTATGAACGAACATTAAGTACGAGATGGCGGACTTGTGAAATTCGTTCAGATATA 600
601 AATTATATGAAGACAAGTTCGTCTACAGAGTCGAATACAAAGGTAGTAATCTCCAGAT 660
601 AATTATATGAAGACAAGTTCGTCTACAGAGTCGAATACAAAGGTAGTAATCTCCAGAT 660
661 GATGTCGCCGTATGCGAGAACTATCTAGAAATAGAGCTTCAATTTGAAGCATATGTAC 720
661 GATGTCGCCGTATGCGAGAACTATCTAGAAATAGAGCTTCAATTTGAAGCATATGTAC 720
721 ATGAATATATGCGCTTTGCTGGCGAAGTAATCTTGTCTATTAATCAATCTCGGAAA 780
721 ATGAATATATGCGCTTTGCTGGCGAAGTAATCTTGTCTATTAATCAATCTCGGAAA 780
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841 TCGTATCATTTTATTCACATCGTTTGGAAAAGACCTTAGTAAGACGGGGGCTTCGTT 900
841 TCGTATCATTTTATTCACATCGTTTGGAAAAGACCTTAGTAAGACGGGGGCTTCGTT 900
901 GAACGACATGAGACGTGCTATGCTCAATGACATCTATAGAGAAACCACTAGATCCTTA 960
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961 CACGATGGGTTTAAACACAGTACATTTCTTTCATATGCTGTTCATGTCGAATATA 1020
961 CACGATGGGTTTAAACACAGTACATTTCTTTCATATGCTGTTCATGTCGAATATA 1020
1021 TATTTTAAACAAATTAATCAATGTTTGTGATATGTTTGTAAACCAATGTTTGTAA 1079
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RESULT 2
US-09-277-716-15
: Sequence 15, Application US/0927716A
: Patent No. 6232107
: GENERAL INFORMATION:
: APPLICANT: Bryan, Bruce
: APPLICANT: Szent-Gyorgyi, Christopher
: APPLICANT: PROLOME, LTD.
: TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
: CURRENT APPLICATION NUMBER: US/09/277,716A
: EARLIER APPLICATION NUMBER: 60/102,939
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: EARLIER FILING DATE: 1998-10-01
: EARLIER APPLICATION NUMBER: 60/089,367
: EARLIER FILING DATE: 1998-06-15
: EARLIER APPLICATION NUMBER: 60/079,624
: EARLIER FILING DATE: 1998-03-27
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 15
: LENGTH: 1079
: TYPE: DNA
: ORGANISM: Renilla mulleri
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (259)..(975)
: FEATURE:
: OTHER INFORMATION: Renilla mulleri Green Fluorescent Protein (GFP)
US-09-277-716-15

Query Match          98.4%  Score 1061.4: DB 4: Length 1085;
Best Local Similarity 99.4%: Pred. No. 1,6e-266;
Matches 1078; Conservative 0; Mismatches 1; Indels 6; Gaps 1;

1  GGTATATACACAGTGATATCGCGGATATCTGCAGACGCATCTAGTGGATATATGAGCGGTA 60
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61  GATATATACGTCAGACCTGCTGTATTCGAACCCACACAACTCTTAATAATAGCCACATTT 120
121  ACATATATCTAAGAGACGCGCTCATTTAAGAGTAGTAAATATATATATATATAGTAGTA 180
121  ACATATATCTAAGAGACGCGCTCATTTAAGAGTAGTAAATATATATATATATATAGTAGTA 180
181  TACAACCTCGCCCTTAGACAGACAGTGTGCACACAGAGTAACCTCTGTTAATGCAATCGAA 240
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301  ATGTGCTATTAATGAATCTGGAAGAAATGTAAACACCATGTTTTCATATGAGAGGT 360
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541  ATGTATGAACGAACATTAAGTACGAGATGGCGGACTTGTCAATATGCTTCAGATATA 600
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721  ATGAATATATGCGCTTTGCTGGCGAAGTAATCTTGTCTATTAATCAATCTCGGAAA 780
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[illegible][illegible]


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US-09-609-161B-31
: Sequence 31, Application US/09609161B
: Patent No. 6436582
: GENERAL INFORMATION:
:   APPLICANT: Bryan, Bruce
:   APPLICANT: Szent-Gyorgyi, Christopher
:   APPLICANT: PROLUME, LTD.
:   TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUC
:   TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIC
:   TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
:   FILE REFERENCE: 24/29-121B
:   CURRENT APPLICATION NUMBER: US/09/609,161B
:   PRIOR FILING DATE: 2000-06-30
:   PRIOR APPLICATION NUMBER: 09/277,716
:   PRIOR FILING DATE: 1999-03-26
:   PRIOR APPLICATION NUMBER: 60/102,539
:   PRIOR FILING DATE: 1998-10-01
:   PRIOR APPLICATION NUMBER: 60/089,367
:   PRIOR FILING DATE: 1998-05-15
:   PRIOR APPLICATION NUMBER: 60/079,624
:   PRIOR FILING DATE: 1998-03-27
:   NUMBER OF SEQ ID NOS: 32
:   SOFTWARE: PatentIn Ver. 2.0
:   SEQ ID NO 31
:   LENGTH: 1279
:   TYPE: DNA
:   ORGANISM: Pilosarcus gurneyi
:   FEATURE:
:   NAME/KEY: CDS
:   LOCATION: (7)..(720)
:   OTHER INFORMATION: Pilosarcus Green Fluorescent Protein (GFP) (Insert B)
: US-09-609-161B-31
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Best Local Similarity 71.2%: Pred. No. 1.3e-92:
Matches 517: Conservative 0: Mismatches 209: Indels 0: Gaps 0:
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OY 313 GTAATCTGGAAGAAATTTTAAACCAATGTTTACAAATGGAAGGTTGCGGCAAAAGG 372
DB 61 GCTAGCGTTGAAGAAATGCTGAACATTCACGTTTTCATGGAAGGATTTGGAAGAGC 120
OY 373 AATATTATTTCGGCAATCACTGTTTCAGATTCGTCGACGAAGGGCCCACTGCTC 432
DB 121 AATGATTTATTGGAAACCAATTTGATGCAAAATCCGGGTTACAAAGGAGGTCGTTGCCA 180
OY 433 TTTCATTTGATATTGTGCACGACCTTTCAATATGCGACGCTTTCACGAATAT 492
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OY 553 ACATTACGTTAGCAAGATGCGGCACTTTTGAATTCGTTCCAGATTAATAATTAGAA 612
DB 301 AATCTAGGCTTTGGAAGATGCGCCACTGTTGACATTCGTTGAGATTAAGATTAGAAAT 360
OY 613 GACAAGTCTGTACAGATTCGAATACAAAGTAGTAACCTCCACAGATGATGTCGCCGTC 672
DB 361 GATTAAGTTCACACTACAAATGAGATATACAGCCAAAGGTTTCCCTGATGAAGGACCCGTC 420
OY 673 ATGCAAGACACTACTTAGGAATAGAGCCCTTCAATTTGAAGCCATGATCAATGAATAGGC 732
DB 421 ATGCAAAAGCCATCTTCGCAATGAGCATGCGTTTGAGCTGCTACTACATGAAGACAGCGC 480
OY 733 GTCCTGGTGGCGGAGTAATCTTCTCTATTAACCTAAGCTGGGGAATATTAATCATGT 792
DB 481 GTTCTGGTGGCGGAGTAATCTTCTCTATTAACCTGAGATGAGGGAATATTAATCATGTGC 540
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OY 793 CACATGAAACATTAATGAAGTCGAAGGTTAGTAAGAGTTTCTCGTATCATTT 852
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OY 853 ATTCAACATCGTTTGGAAAAAGACTTACGTAGAAGAGGGGGGTTCTGTTGAACAGATGAG 912
DB 601 ATCCATCATCTGCTGGAGAAAACCTACGTTGAAGGAAGAGGCTTCTGGAAACACGAG 660
OY 913 ACTGCTATTGCTCAATATGACATTTATAGAAAACCACTAGATTCCTTACACGAATGGTT 972
DB 661 ACGGCGATTCACACACTGACACCAATTTGAAAACCTTGCGCTCCCTCATATGATGGGTG 720
OY 973 TAAACA 978
DB 721 TAGAAA 726
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```
RESULT 7
US-09-956-7
: Sequence 7, Application US/09459956
: Patent No. 6342379
: GENERAL INFORMATION:
:   APPLICANT: Tslen, Roger Y.
:   APPLICANT: Gonzalez, Jil, Jesus E.
:   TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
:   TITLE OF INVENTION: OPTICAL METHODS
:   FILE REFERENCE: REGEN1290-4
:   CURRENT APPLICATION NUMBER: US/09/459,956
:   CURRENT FILING DATE: 1999-12-13
:   PRIOR APPLICATION NUMBER: 08/765,860
:   PRIOR FILING DATE: 1999-05-08
:   PRIOR APPLICATION NUMBER: 08/481,977
:   PRIOR FILING DATE: 1995-06-07
:   PRIOR APPLICATION NUMBER: PCT/US96/09652
:   PRIOR FILING DATE: 1996-06-06
:   NUMBER OF SEQ ID NOS: 22
:   SOFTWARE: FastSeq for Windows Version 4.0
:   SEQ ID NO 7
:   LENGTH: 801
:   TYPE: DNA
:   ORGANISM: Clavulatia sp
: US-09-956-7
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Best Local Similarity 56.1%: Pred. No. 6.5e-33:
Matches 325: Conservative 0: Mismatches 251: Indels 3: Gaps 1:
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OY 353 TGGAGGCTTGGCGCAAGGAATATTTATTCGGCAATCACTGTTCAAGATTCGTCA 412
DB 200 TCGAAGGAGGAAGGAGGAAGGAAGCCCTTACGATGGGACACACTTTAAACCTGGAAGTGA 259
OY 413 CGAAAGGGGCGCCACTGCTTTTTCATTTGATATGTCGACACAGCTTTTCATATAGCA 472
DB 260 AGGAAGTCCGCTCTGCTTTTTCATTTTTCATTTTTCATTTTTCATTTTTCATTTTTCAT 319
OY 473 ACCGTAATCTTCAAGAAATTCGAATGATATATCAGATTAATTTTATACATCAATTCAG 532
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OY 533 CAGGATTTATGATGAGCAACATTAATTTACGAGATGCGGCACTGTTGAATTCGTT 592
DB 380 AGGATATTTCTGCGAAGAACCATGACTTTTGAAGACAAAGCATTTGCAAGATGAGAAA 439
OY 593 CAGATTAATTAATTAATGAGAACAGATTCGCTACAGAGACTGCAATACAAAGATGACT 652
DB 440 GTGACATTAAGCATGAGGAGAGACTCCTTTATCTATGAATTTGCTTTGATGAGGATGACT 499
OY 653 TCCACATGATGATGCTCCGTCATGACGAGAGACATATCTTAGAATAGAGCCATTTGAAG 712
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Db 500 TTCCTCCCAATGGTCCGGTTATGACAGAAAAAATTGGAAGTGGGAACCATCCACTGAGA 559
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Db 560 TTATGACCTGGTGATGATGAGTGTGTGCGAGATATTTGCCATTCCTGTTGCTGGAGG 619
Qy 773 CTGGGAATATTTATTCATCTCATGAAAAATTAATGAGTCGAAGGTGTAGTAAAG 832
Db 620 GAGGTGGCATTAACCATGTGACTGTCAAAAGATATTACAAAGAAAAAAGTTGTCA--- 676
Qy 833 AGTTTCCTTGATATCATTTTATTTCAACATCGTTTGAAG 871
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RESULT 8

US-09-459-956-5
; Sequence 5, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Gonzalez, III, Jesus E.
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
; FILE REFERENCE: REGEN1290-4
; CURRENT APPLICATION NUMBER: US/09/459,956
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 08/765,860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481,977
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09652
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Discosoma striata
US-09-459-956-5

Query Match 12.8%; Score 138.6; DB 4; Length 699;
Best Local Similarity 51.9%; Pred. No. 5,1e-27;
Matches 337; Conservative 0; Mismatches 309; Indels 3; Gaps 1;
Qy 280 AACACTTGTTTACAGAAATATGCTGATTAAGTAATCTGGGAAGCAATTTGAAACAAC 339
Db 13 AAGAGTGTGATCAGAGGAAGAAATGTTGATCGATCTTCATCTCGAAGGAACGTTCAATGGG 72
Qy 340 CATGTTTTTACATGAGAGGTTGCGCAAGGAATATTTTATTCGCAATCAACTGGTT 399
Db 73 CACTTACTTTGAATATAAAGCAAGGAAGGAAGGACGCTTAATGAGGCCAATACCGTTC 132
Qy 400 CAGATTCGTGTCAGAAAGGGGCCCATGCTTTTGCATTTGATATTTGTCACCAAGCT 459
Db 133 ACGCTCGAAGTTACCAAGGCTGACCTTCGCATTTGTTGGCATTTTGTGGCCACAA 192
Qy 460 TTTCATATGGAACCGTACTTTACAGAAATATCCGAATGATATATACATTAATTTATA 519
Db 193 TTTTCAGTATGGAAGCAAGGCAATTTGTCCACACCCCTGACAAACATATCATTAATYCTAAG 252
Qy 520 CATCATTTTCCAGAGAGATTTATGTAAGCAACATTTACGTACGAAGATGGCGACTT 579
Db 253 CTGTCAATTTCCGAGAGGATATACATGGAACGGTCCATGACTTTTAAACGCTGGCTTG 312
Qy 580 GTTGAATTCGTTGAGATATAAATTTAATAGAAGCAAGTTGCTTACAGAGTGAATAC 639
Db 313 TGTGTATCACCAGATGATATCAAGTTGACAGGCAACTGTTTCTACACACATCAAGTTTC 372
Qy 640 AAGGTAGTAACCTCCCAATGATGCTCCGTCATGACAGACATATCTTAGGAATAGAG 699
Db 373 ACTGGCTGAACCTTCTCCAAATGAGACCCGTTGTGACAGAGAGCAACATGCTGGCGAA 432

Qy 700 CCTCATTTGAAGCCATGATACATGAATTAATGGCGCTTGTGCGGAAGTAATTCCTTTC 759
Db 433 CCGAGACACTGAGCGTTTGTATCTCTGATGATGGTGTATTATAGAGACATTCATGCT 492
Qy 760 TATTAACATAACTCTGGGAATATTTATTCATGTCACATGAAGAAATTAATGAAGTCGAAA 819
Db 493 CTGACAGTTGAAGAGAGGTGCTCATACCATGTGACATTAACACTGTATTACAGGGCGAAG 552
Qy 820 GGTGTAGTAAGAGATTTCTTCGTATCATTTTATTTCA---ACATGCTTTGGAAAAAGCT 876
Db 553 AAGGCCGCTTGAAGATGCGCAGGTATTCATATGTTGAACCAAACTGGTTATATGGAAC 612
Qy 877 TAGCTAGAAGACGGGGGTTGCTTGAACAGCATGAGACTGCTATTGGCTC 925
Db 613 AACGACAAAGATTCATGAAGTTGAGAGCATGAATCGCCGTTGCAC 661

RESULT 9

US-09-459-956-6
; Sequence 6, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Gonzalez, III, Jesus E.
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
; FILE REFERENCE: REGEN1290-4
; CURRENT APPLICATION NUMBER: US/09/459,956
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 08/765,860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481,977
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09652
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Discosoma sp
US-09-459-956-6

Query Match 12.5%; Score 134.8; DB 4; Length 678;
Best Local Similarity 50.8%; Pred. No. 4,9e-26;
Matches 322; Conservative 0; Mismatches 312; Indels 0; Gaps 0;
Qy 280 AACACTTGTTTACAGAAATATGCTGATTAAGTAATCTGGGAAGCAATTTGAAACAAC 339
Db 13 AAGAAATGTTATCAGAGAGTTATGATGAGCTTTAAGGTTCCGATGGAAGAACGGTCAATGGG 72
Qy 340 CATGTTTTTACATGAGAGGTTGCGCAAGGAATATTTTATTCGCAATCAACTGGTT 399
Db 73 CAGGAGTTTGAATATAAAGCAAGGAAGGAGGAGCCATACCAAGGCCACATATCCGTA 132
Qy 400 CAGATTCGTGTCAGAAAGGGGCCCATGCTTTTGCATTTGATATTTGTCACCAAGCT 459
Db 133 AAGCTTAAGGTAAACCAAGGGGGGACCCTTTGCCATTTTGGTATTTTGTGCACCAAA 192
Qy 460 TTTCATATGGAACCGTACTTTACAGAAATATCCGAATGATATATACATTAATTTATA 519
Db 193 TTTTCAGTATGGAAGCAAGGATATATGTCAGACACCCCTGCGACATATACAGATATAAAG 252
Qy 520 CATTCATTTCCAGAGAGATTTATGTAAGCAACATTTACGTACGAAGATGGCGACTT 579
Db 253 CTGTCAATTTCCGAGAGGATTTAATGGAAGGTCATGAACCTTTGGAACACGCTGGCGTC 312
Qy 580 GTTGAATTCGTTGAGATATAAATTTAATAGAAGCAACGTTGCTTACAGAGCTGCAATAC 639
Db 313 GTTACTGTAAACCCAGAGATTCAGTTTGGACAGATGGCTGTTTATCTTCAAGAGCTCAAGTTTC 372
Qy 640 AAGGTAGTAACCTCCCAATGATGCTCCGTCATGACAGACATATCTTAGGAATAGAG 699

```
Dh 373 ATTGGCTGAACCTTCCTCCGATGACCTGTTATGCAAAAGACATGGGCTGGAA 432
Qy 700 CCTCATTTGAAGCCATGATCATGAATATGGCTCTGGCGAGATATTTCTTGTC 759
Dh 433 GCCGAGCACTGACGCTTGATTCCTCGATGATGGCTGTTGAAAGAGAGATTCATTAAGCT 492
Qy 760 TATAAATAAAGCTCTGGGAAATATTTATTCATGTCATGAACCAATTAATGAAGCTGAAA 819
Dh 493 CTGAAGCTGAAGACGCTGCTGATTAACCTAGTGAATTCAAAGATTTACATGGCAAG 552
Qy 820 CGTGTACTAAGAGGATTTCCCTTCGATCATTTTATTAACATCGTTTGGAAAGACTTAC 875
Dh 553 AAGCTGTGAGCTACCGAGGCTACTACTATGTTGACCTCCAAACTGGAATATACAGCCAC 612
Qy 880 GTAGAAGCCGGGGTCTGTTGAACAGCATGAGA 913
Dh 613 AACCAAGACTATACATCGTTTGACAGCATATGAAA 646
```

```
RESULT 10
US-09-459-956-2
: Sequence 2, Application US/09459556
: Patent No. 6342379
: GENERAL INFORMATION:
: APPLICANT: Tsien, Roger Y.
: APPLICANT: Gonzalez, III, Jesus E.
: TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
: TITLE OF INVENTION: OPTICAL METHODS
: FILE REFERENCE: REGEN1290-4
: CURRENT APPLICATION NUMBER: US/09/459,956
: CURRENT FILING DATE: 1999-12-13
: PRIOR APPLICATION NUMBER: 08/765,860
: PRIOR FILING DATE: 1999-05-08
: PRIOR APPLICATION NUMBER: 08/481,977
: PRIOR FILING DATE: 1995-06-07
: PRIOR APPLICATION NUMBER: PCT/US96/09652
: PRIOR FILING DATE: 1996-06-06
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 690
: TYPE: DNA
: ORGANISM: Anemonia majano
US-09-459-956-2
```

```
Query Match 11.4% Score 123.2; DB 4; Length 690;
Best Local Similarity 52.2% Pred. No. 5.1e-23;
Matches 350; Conservative 0; Mismatches 308; Indels 12; Gaps 3;
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Qy 280 AACACTTGTTTACAGAGATATGCTGATTAAGTAATCTGGAAGGATTTGTAACGAC 339
Dh 13 AACAGCTTTATCGGAGATGACATGAATGACCTACCATATGATGCTGTGTCATGGG 72
Qy 340 CATGTTTTCATGAGGCTTCGGCAAGAGAAATATTTATTCGGCAATCAACTGGTT 399
Dh 73 CATTACTTTACCTCAAGCTGAAGGCAAGGAGCCATACGAGGAGCCAGACTTCG 132
Qy 400 CAATTTCGTGCA-----CGAAAGGGGCGCCACTGCTTTTTCATTTGATATTTGTC 453
Dh 133 ACTTTTAATCTACATGCGCAACGGTGGGCCCTTGCAATTTCTTTGACATACATCT 192
Qy 454 CGAGCTTTTCATATGCAACCTGACTTTTCAGCAATATCCGAATATATTCAGATTAT 513
Dh 193 ACGGTGTTCATATGCAATATGCAATGATGCTTTACTGCGTATCTTACCAATATGCGCGACTAT 252
Qy 514 TTTATACATTCATTTTCAGCAGATTTATATGAGCAAGCAATTTACCTTTCAGAAATGCG 573
Dh 253 TTTCAACCAACATTTTCTGAGCAATGTCATATGAAAGCACTTTTACCTTATGAAGATGGA 312
Qy 574 GGAAGCTGTGAATTCGTTGAGATATTAATTTATAGAACCAAGTTGCTGACAGAGTC 633
Dh 313 GGAGTTGCTACAGCCAGTTGGAAATAGGCTTAAGGCAACATTCCTTTAGGACACAAATCC 372
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Qy 634 GAATACAAAGGTAGTAACTTCCAGATGATGTCGCCGTCAATGCAAGAGACTATCTTAGGA 693
Dh 373 ACGTTTCATGAGAGCACTTTCCCTCGATATGAGACTTGTGATGGGAAGAACACATGCT 432
Qy 694 ATAGAGCCTTCATTTGAAGCCATGTACATGATATATGCGCTCTTGTCGGCGGAATATT 753
Dh 433 TGGGACCACTCTTTTGAAGAAATGACTGCTGCGATGGAATATGAAGGCTGATGTCACC 492
Qy 754 CTGTGTATTAACATAAATCTCGGGAATATTTATTCATGTCACATGAAACATTAATGAAG 813
Dh 493 GCGTTCCTCATGCTGCAAGAGAGTGCCAAATTCAGATGCCAATTCACACTCTTTACAG 552
Qy 814 TCGAAAGGTAGTAAAGAGATTTCCCTTCGATCATTTTATTCACATTCGTTGGAAAG 873
Dh 553 ACAAAGAAACCGGTGAGAGAT---CCACCAACCATGTGCTGGACATTCGCATTGCCAGC 609
Qy 874 ACTTACCTAGAGAGCGGGGGTCTGTTCAACAGCAT--GAGACTGCTATTGCTCAATG 930
Dh 610 ACCGACCTGACAAAGGTGCAACAGCTGTTCAGCTGACGAGCAGCGTGTTCACATATA 669
Qy 931 ACATCTATAG 940
Dh 670 ACCTCTGTTG 679
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RESULT 11
US-09-459-956-4
: Sequence 4, Application US/09459556
: Patent No. 6342379
: GENERAL INFORMATION:
: APPLICANT: Tsien, Roger Y.
: APPLICANT: Gonzalez, III, Jesus E.
: TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
: TITLE OF INVENTION: OPTICAL METHODS
: FILE REFERENCE: REGEN1290-4
: CURRENT APPLICATION NUMBER: US/09/459,956
: CURRENT FILING DATE: 1999-12-13
: PRIOR APPLICATION NUMBER: 08/765,860
: PRIOR FILING DATE: 1999-05-08
: PRIOR APPLICATION NUMBER: 08/481,977
: PRIOR FILING DATE: 1995-06-07
: PRIOR APPLICATION NUMBER: PCT/US96/09652
: PRIOR FILING DATE: 1996-06-06
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 696
: TYPE: DNA
: ORGANISM: Zoanthus sp
US-09-459-956-4
```

```
Query Match 9.6% Score 103.2; DB 4; Length 696;
Best Local Similarity 55.5% Pred. No. 7.9e-18;
Matches 223; Conservative 0; Mismatches 173; Indels 6; Gaps 1;
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Qy 287 GTTTACAAAGAGATATGCTGATTAAGTAATCTGGAAGGAAATTTGTAACACCATGTTT 346
Dh 20 GTCTTAAGAGAAATGATCAATGAAATACCAATGGAAGGCTGCTTAACGACATTAAT 79
Qy 347 TTCAATGAGAGCTTGGCGCAAGGCAATATTTTATTCGGCAATTCAACTGTTTCAGATTG 406
Dh 80 TTTGATCAGAGGCGGAAGGATTTGATATTCGTTTCAAGGAAAGACATTAATATCTGT 139
Qy 407 GTGTACAGAAAGGGGCGCCACTGCTCTTTGCAATTTGATATTTGTCACGCTTTTCAAT 466
Dh 140 GTGTGATCGAAGGGGCGCCATTTGCCATTTTCCGAAGCAATATTTGTCAGCTGCTTAAGT 199
Qy 467 ATGCAACCGTACTTTCAGCAATATTCGGAATGATATAGATATTTATTAATATTCAT 526
Dh 200 ACGGAGACAGGATTTTACGATATATCTTCAGACATAGTAGACTATTTCAAGAACTCGT 259
Qy 527 TTCAGAGGATTTATGATATGAACGAACATTTACGTTACGAAGATGCGGACTGTGAAA 586
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Db 260 GTCCTCGATATACATGGGCGAGCTCTTCTTTGAGATGGAGCAGTCTGATAT 319
QY 587 TTGCTTCAGATATA-----AATTATAGAACACAGTTCGCTACAGAGTGATACA 640
Db 320 GCATGTAGATATACAGTGCAGTGTCAAAAGAACTGATTTATCATAGAGATATTTA 379
QY 641 AAGTAGTACTTCCAGATGATGTCCTCATGCGACAGAGA 682
Db 380 ATGGAATGAATTTCTCTGATGACCTGTGATGAAAAAGA 421

RESULT 12

US-09-459-956-3
; Sequence 3, Application US/094595956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Gonzalez, III, Jesus E.
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
; FILE REFERENCE: OPTICAL METHODS
; FILE REFERENCE: REGEN1290-4
; CURRENT APPLICATION NUMBER: US/09/459,956
; CURRENT FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 08/765,860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481,977
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09652
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Zoanthus sp
US-09-459-956-3

Query Match 9.0%; Score 97.6; DB 4; Length 696;
Best Local Similarity 53.5%; Pred. No. 2.3e-16;
Matches 230; Conservative 0; Mismatches 194; Indels 6; Gaps 1;

QY 287 GTTTACAGAGTAATGTCTATTAAGTAATCTGGAAGGAATTTGAACACCATGTTT 346
Db 20 GTCTACAAAGAAATGACATGAATATACCGTATGGAAGGTCGCGATGACATTAAT 79
QY 347 TTACATGAGGTTGCGGCAAGGAATTTTATTCGGCATCACTGTTACAGATTTC 406
Db 80 TTGTGATCAGGAGGAGGCGATTGATATCCGTTCAAAAGGGAACAGGCTATTATCTGT 139
QY 407 GTGTACGAAAGGGGCCCTGCTTTGATTTGATATGTCACCGCTTTTCAT 466
Db 140 GTGTGTCAGAGGTGACACCTTTCATTTCCGAAAGCAATTTGTCAGCTGCTTTACT 139
QY 467 ATGGCAACCGTACTTTCACGAAATATCCGAATGATATATGATTTTATTCATCAT 536
Db 200 ACGGAACAAGGGTTTTCAGTGAATATCTCAAGACATAGTTGACTTTTCAAGACTGT 259
QY 527 TTCCACAGAGATTATGTATGACGAACATTAAGTTACGAAGATGGGCGCTGTGAAA 586
Db 260 GTCTCTCGATATACATGGGACAGGCTTTTCTTTTGAGATGGGCGCTTTGCAATAT 319
QY 587 TTGCTTCAGATATA-----AATTATAGAGAACAGTTCGCTACAGAGTGCAATACA 640
Db 320 GTATATGACATATACAGTGCAGTGTGGAAGAAACAGTATGATCATGATGATCAAAATTTT 379
QY 641 AAGTAGTACTTCCAGATGATGTCCTCATGCGACAGAGAAGTATCTTGAATAGAGC 700
Db 380 ATGGAATGAATTTCTCTGATGACCTGTGATGAAAAAGATGACGATTAAGTGGGAGC 429
QY 701 CTTCATTTGA 710
Db 440 CATCTGCGA 449

RESULT 13

US-08-672-158A-20
; Sequence 20, Application US/08672158A
; Patent No. 5770371
; GENERAL INFORMATION:
; APPLICANT: Sheryl Thompson
; TITLE OF INVENTION: Modification of Cryptic Splice Sites In
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 57703710 No. 5770371disk of No. 5770371th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,158A
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Agis Dr., Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 4855,000-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 751 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-672-158A-20

Query Match 4.6%; Score 50; DB 1; Length 751;
Best Local Similarity 49.5%; Pred. No. 0.00053;
Matches 190; Conservative 0; Mismatches 185; Indels 9; Gaps 2;

QY 288 TTTTACAGAGTAATGTCTATTAAGTAATCTGGAAGGAATTTGAACACCATGTTT 347
Db 21 TTTCAGTGGAGTTGTCCCAATCTCTTGAATTTAGATGGGATGTAATGGGCAAAATTT 80
QY 348 TACAATGAGAGGTTGGGCAAGGAATATTTATTCGGCAATCACTGTTGCAATTCG 407
Db 81 CTCTGTAGTGGAGAGGTTGAAGGTGATGACATACGGAACCTTAACCTTAATTTAT 140
QY 408 TGTACGAAAGGGGCCCTGCTTTGATTTGATTTGTCACAGCTTTTCAATA 467
Db 141 TTTCAGTACAGG---AAGCTACCTGTTCATGTCACAGCTTGTGTCATTTCTCTTA 197
QY 468 TGGCAACCGTACTTTCACGAAATATCCGAATGATATATCA-----GATTATTTTATACA 521
Db 198 TGGTGTTCATAGCTTTTTCAGATACCCAGATCATATGAAACACAGTACTTTTTCAGAG 257
QY 522 ATCATTTCCAGCAGATTATGTATGACGACATTCATTCAGTACAGATGGGCGCTTGT 581
Db 258 TGGCATGCCCCGAAGGTTATGTACAGGAAGACATTAATTTTACAAAGATGACGGGAACTA 317
QY 582 TGAATTTGTTTCAGATATTAATTTAATAGAGCAAGTTCGTCACAGAGTGCATACAA 641
Db 318 CAGACACAGTGTGAGAGTCAAGTTTGAAGGTATACCTTTGTTAATAGATGAGTTAAA 377
QY 642 AGGTAGTACTTCCAGATGATGG 665
Db 378 AGGTATTTGATTTTAAAGAGATGG 401

```

RESULT 14
US-08-452-295-2
: Sequence 2, Application US/08452295
: Patent No. 5741668
: GENERAL INFORMATION:
:   APPLICANT: Ward, William W.
:   TITLE OF INVENTION: A BIOLUMINESCENT INDICATOR FOR GENE
:   TITLE OF INVENTION: EXPRESSION AND DETECTION OF MUTAGENESIS BASED UPON THE
:   TITLE OF INVENTION: EXPRESSION OF A GENE FOR A MODIFIED GREEN-FLUORESCENT
:   NUMBER OF SEQUENCES: 5
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: Omri M. Behr, Esq.
:     STREET: 325 Pierson Avenue
:     CITY: Edison
:     STATE: New Jersey
:     COUNTRY: USA
:     ZIP: 08837
:   COMPUTER READABLE FORM:
:     MEDIUM TYPE: floppy disk
:     COMPUTER: IBM PC compatible
:     OPERATING SYSTEM: PC-DOS/MS-DOS
:     SOFTWARE: Patent Release #1.0, Version #1.25
:     CURRENT APPLICATION DATA:
:       FILING DATE: 26-May-1995
:       CLASSIFICATION: 435
:       ATTORNEY/AGENT INFORMATION:
:         NAME: Behr, Omri M.
:         REGISTRATION NUMBER: 22,940
:         REFERENCE/DOCKET NUMBER: PUTG3.0-017
:         TELECOMMUNICATION INFORMATION:
:           TELEPHONE: (908) 494-5240
:           TELEFAX: (908) 494-0428
:           TELEX: 51 1642 BEPAIDEN
:           INFORMATION FOR SEQ ID NO: 2:
:             SEQUENCE CHARACTERISTICS:
:               LENGTH: 944 bases
:               TYPE: nucleic acid
:               STRANDEDNESS: both
:               TOPOLOGY: linear
:             MOLECULE TYPE: cDNA
: US-08-452-295-2

Query Match          4.6%      Score 50; DB 1; Length 944;
Best Local Similarity 45.5%; Pred. No. 0.00058;
Matches 190; Conservative 0; Mismatches 185; Indels 9; Gaps 2;

OY    288 TTTACAAAGACTATGTCTGATAAAGTAATTCGGGAAGGAATTGTAAACACCAGTCTTT 347
Db    24  TTCTACTGCAGACTTGCCCAATTCCTGTGTGAATTAGAATGGCATTTAATGGCAAAAT 83

OY    348 TACAATGAGGGGTTCGCCGAAGGGAATATTATTTCGCCGATCAACTGGTTAGATTGG 407
Db    84  TTCCTGAGTGCAGAACGGGTGAGGTGATGACATACCGGAAGAACTTAGCCTTAATTAT 143

OY    408 TGCTACGGAAGGGCCCCACTGCTTTTGGCATTTGATATTGTGTCAACGACCTTTTAATA 467
Db    144 TTGCACTACTGG--AAACACTACTGTTTCATGCGCACACACTGTGACTACTTTCTATTA 200

OY    468 TGCGAACCGCTACTTTCACGCAATATCCGATCGATATATCA-----GATTTATTATACA 521
Db    201 TGGTGTTTCATGCTTTTTCACGATACCCGATCAITATGAAGACACATGACTTTTTCAGAG 260

OY    522 ATCATTTCCAGCAGGATTTATGATGAAACGACATTACGTTAGAGAGATGGCGGACTTGG 581
Db    261 TGCCATGCCCAAGGATATGATGACAGGAAGACATATATTTTCAGAGATGACGGGAAGTA 320

OY    582 TGAATTTGCTTCACATATTAATTTAATAGAAAGACAACTTCGCTCACAGAGTCGAATACAA 641
Db    321 CAAGCAGGCTCTGAACTCAAGTTTGAAGGTGATACCTTGTTAATAGAAATGACAGTTAAA 380

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RESULT 15

US-09-380-190A-18
Sequence 18, Application US/09380190A
Patent No. 6410220

GENERAL INFORMATION:
APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES THEREOF

NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: MUEITING, RAASCH & GEBHARDT, P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MINNESOTA
COUNTRY: USA
ZIP: 55401

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/380,190A
FILING DATE: 26-Aug-1999
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/03918
FILING DATE: 28-FEB-98
ATTORNEY/AGENT INFORMATION:
NAME: MEETING, ANN M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 228.00010201

TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:
LENGTH: 5754 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-380-190A-18

Query Match 4.6%; Score 50; DB 4; Length 5754;
Best Local Similarity 49.5%; Pred. NO. 0.0011;
Matches 190; Conservative 0; Mismatches 185; Indels 9; Gaps 2

DG 288 TTTACAGAAGTAATGTCTGATAAAGTAATCTCGAGAAATTGGTAACAACCATTGTTT 347
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
DB 1578 TTTCACAGGAGTGTCOCCAATCTGTGTGAATTAGATGTGATGTAATAGGCACAAAAT 1637

DG 348 TACCAATGGAGGGCTTCGCCAAGAAGCATATTTTATTTCGGCAATCAACTGGTTCAGATTG 407
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
DB 1638 TTCGTGCAATGTGAGAAGGCGTAGAGTGATCCACACATACGAAAACTTACCCTTAATTAT 1697

DG 408 TCCTCACGAAGGGGCCCACTGCGCTTTTCGATTTGATATGTGTACACAGCTTTTCAATA 467
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
DB 1698 TTGCACACTACTGG---AAACTACTGTTCCACAGGCCAACACTTGTACTACTTACTTA 1754

DG 468 TGCGAACCGCTACTTTCACGAATATCCGAATGATATGATGCA-----GATTATTTATACA 521
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
DB 1755 TGGCTTTCATATCTTTTACAGATATCCCAGATATATGAAACGGCATGCTTTTTCACAG 1814

DG 522 ATCATTTCCAGCAGGATTATATGATGAACGACATTACGTTACGAAAGATGGCGGACTGT 581
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1815 TGCATGCCCGAAGGTTATGTACAGGAAGAACTATATTTTCAAGATGACGGAACTA 1874
QY 582 TGAATTCGTTCAATATTAATTAATAGACAAGTTGCTACAGATCGAATACAA 641
Db 1875 CAAGACACGTGCTGAAGTCAAGTTGAAGTGATACCTTGTTAATAGAAATCGAGTTAA 1934
QY 642 AGTAGTAACCTTCCAGATGATGG 665
Db 1935 AGTATTGATTTAAGAAAGATGG 1958

Search completed: January 16, 2003, 11:04:09
Job time : 65.946 secs

According to the Pre Publication Rules, every patent application received by the United States Patent and Trademark Office after November 29, 2000 will be pre-published at eighteen months from the effective filing date. When the application is published the contents, including the sequences, will become prior art.

Two new databases have been created to hold the pre-published sequences:

Published_Applications_NA contains nucleic acid sequences; the search results will have the extension **.rnpb**.

Published_Applications_AA contains amino acid sequences; the search results will have the extension **.rapb**.

Each pre-published application is given a unique Publication Number. An example of a Publication Number is US20021234567A1. The "US" indicates the application was a U.S. application. The first 4 digits show the calendar year the application was published. The next 7 digits represent when the application was published. This 7-digit number starts at zero at the beginning of each calendar year. Each application published is given the next number in order. The "A" indicates a utility patent application and the "1" shows that this was the first time the application had been published. If the applicants submit changes to the application, they may request that the changed application be published again. In such instances, the "1" at the end of the number would be replaced by a "2".

Sequences in the PGPub database are public information; it is permissible to leave these results in the case.

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OM nucleic - nucleic search, using sw model

Run on: January 15, 2003, 12:06:25 : Search time 58.8186 Seconds
(without alignments)
8179.248 Million cell updates/sec

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Perfect score: 1079
Sequence: 1 ggtatacacaagtgatcgcgttgcgttcacaaagggtccgcgttcattt 1079

Scoring table: IDENTITY_MUC
Gapop 10.0, Gapext 1.0

Searched: 393868 seqs, 222934149 residues

Total number of hits satisfying chosen parameters: 787736

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq:*

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7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

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10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

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14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	462.4	42.5	720	US-10-060-857-3	Sequence 3, Appli
3	390.4	36.2	720	US-10-060-857-4	Sequence 4, Appli
4	368	34.1	720	US-10-060-857-5	Sequence 5, Appli
5	336	31.1	720	US-09-795-040A-3	Sequence 3, Appli
6	336	31.1	720	US-10-060-857-2	Sequence 2, Appli
7	294	27.2	1482	US-09-977-857-1	Sequence 1, Appli
8	161.4	15.0	801	US-09-967-772-7	Sequence 7, Appli
9	161.4	15.0	1116	US-10-006-922-3	Sequence 3, Appli
10	150.5	14.0	850	US-10-006-922-9	Sequence 9, Appli
11	138.6	12.8	699	US-09-967-772-5	Sequence 5, Appli
12	134.8	12.5	678	US-09-967-772-6	Sequence 6, Appli
13	134.8	12.5	678	US-10-006-922-11	Sequence 11, Appli
14	134.8	12.5	859	US-09-999-745-66	Sequence 66, Appli
15	133.6	12.3	908	US-09-976-673-3	Sequence 3, Appli
16	131	12.1	910	US-09-976-673-1	Sequence 1, Appli
17	130.4	12.1	876	US-10-006-922-17	Sequence 17, Appli
18	129.4	12.0	681	US-09-976-673-7	Sequence 7, Appli
19	129.4	12.0	684	US-09-976-673-5	Sequence 5, Appli

20	129.4	12.0	684	US-09-976-673-23	Sequence 23, Appli
21	127.8	11.8	681	US-09-976-673-9	Sequence 9, Appli
22	123.6	11.5	898	US-10-006-922-45	Sequence 45, Appli
23	123.2	11.4	690	US-09-967-772-2	Sequence 2, Appli
24	120.2	11.1	687	US-10-006-922-13	Sequence 13, Appli
25	119	11.0	680	US-09-976-673-25	Sequence 25, Appli
26	115.2	10.7	696	US-10-006-922-13	Sequence 13, Appli
27	103.2	9.6	696	US-09-967-772-4	Sequence 4, Appli
28	103.2	9.6	865	US-10-006-922-7	Sequence 7, Appli
29	100.4	9.3	681	US-10-006-922-35	Sequence 35, Appli
30	99.2	9.2	705	US-10-006-922-29	Sequence 29, Appli
31	98.8	9.2	681	US-10-006-922-37	Sequence 37, Appli
32	98.8	9.2	6984	US-10-001-189-45	Sequence 45, Appli
33	98	9.1	919	US-10-006-922-15	Sequence 15, Appli
34	97.6	9.0	696	US-09-967-772-3	Sequence 3, Appli
35	97.4	9.0	687	US-09-976-673-13	Sequence 13, Appli
36	97.4	9.0	1396	US-09-976-673-15	Sequence 15, Appli
37	97.4	9.0	1424	US-09-976-673-17	Sequence 17, Appli
38	96.8	9.0	675	US-10-006-922-38	Sequence 38, Appli
39	96.8	9.0	678	US-10-006-922-36	Sequence 36, Appli
40	96.8	9.0	1050	US-10-060-857-7	Sequence 7, Appli
41	96	8.9	693	US-10-006-922-5	Sequence 5, Appli
42	95.8	8.9	687	US-09-976-673-11	Sequence 11, Appli
43	90.8	8.4	690	US-10-006-922-27	Sequence 27, Appli
44	89.2	8.3	699	US-10-006-922-41	Sequence 41, Appli
45	84.6	7.8	707	US-10-006-922-39	Sequence 39, Appli

ALIGNMENTS

RESULT 1

US-09-795-040A-1

: Sequence 1, Application US/09795040A

: Patent No. US20020064842A1

: GENERAL INFORMATION:

: APPLICANT: Stratagene

: TITLE OF INVENTION: Renilla Reniformis Green Fluorescent Protein and Mutant's There

: FILE REFERENCE: 25436/1162

: CURRENT APPLICATION NUMBER: US/09795,040A

: CURRENT FILING DATE: 2001-02-26

: PRIOR APPLICATION NUMBER: US 60/185,589

: PRIOR FILING DATE: 2000-02-28

: PRIOR APPLICATION NUMBER: 60/210,561

: PRIOR FILING DATE: 2000-06-09

: SOFTWARE: PatentIn version 3.0

: NUMBER OF SEQ ID NOS: 8

: SEQ ID NO 1

: LENGTH: 720

: TYPE: DNA

: ORGANISM: Renilla reniformis

: FEATURE:

: NAME/KEY: exon

: LOCATION: (1)..(720)

: OTHER INFORMATION: open reading frame

US-09-795-040A-1

Query Match 49.5%: Score 534.4: DB 10: Length 720:

Best Local Similarity 83.9%: Pred. No. 1.2e-110:

Matches 604: Conservative 0: Mismatches 116: Indels 0: Gaps 0:

QY	256	ACGATGAGTAACCAATATTTGGAAGACACTGTTTACAGAACTATGTCGTTAAAGTA	315
DB	1	ATGTGTAGTAACCAATATTTGGAAGACACTGATGATGTCGTTTAAAGTG	60
QY	316	AATCTGAGGAATTTTAAACCAATGTTTACATGAGGCTTGCGGCAAGGAAT	375
DB	61	AATCTGAGGAGTGTAGTAACCAATGTCGTCACATGGAAGCTTGGAAGAAAT	120
QY	376	ATTTTATTCGGAATCACTGTTGATTCGTCGACGAAGGGCCCTGCTTTT	435
DB	121	ATTTTATTCGGAACCACTGTCGATTCGTCGACGAAGGGGTCCGCTTCATT	180

QY	436	GCATTGGATTTGGTCCACCAGCTTTTCATPATGGCAACGGTCTTCCAGCAATATACCG	495
Db	181	GCATTTCATATTTCTCTACCAAGCTTTTCCATATAGGCAACGGTCAATTCAGCAATATACCG	240
QY	496	AATGATATATCAGATTAATTTATATACATATCATTTCCACAGAGATTTATGATATGAAAGACA	555
Db	241	GAGATATATCAGACTTTTATATACATATCTTTCCACGGGATTTGATATGAAACACAG	300
QY	556	TTAGCTTACGAAGATGGCGGACTGGTTGAATTCGTACATATATAATTAATATGAAAGAC	615
Db	301	TTGGCTTACGAAGATGGTGGACGTGGTTGAATTCGTACATATATAATTAATATGAAAGAC	360
QY	616	AACTTCGTCTACAGAGTCGATATACCAAGGTAGTAACCTTCCAGATGATGGTCCCGTATC	675
Db	361	ATGTTTGTCTACAGATGGAAATATAAGTAGTAGTAACCTTCCAGATGATGGTCCAGTAGATC	420
QY	676	CAGAAGACTATCTTAGGAATATAGACCTCTTCACTTTGAAGCCATGTACATGAATATAGCGCTC	735
Db	421	AAGAAGACAATCACAGATTTTACCAACCTTCGTCCGAATTTGTATATAGAACGATGGCGTCC	480
QY	736	TTGTCGCGCGAAGTAATTTCTGTCTATAAACTAAACCTGGGAATATTTATCATGTAC	795
Db	481	TTTGGTTGGCCAAAGTCATTTCTGTTATATAGATTAACCTGGCAAATTTTATTCGTGTAC	540
QY	796	ATGAAACATTATATGAAGTCGAAAGGTGTATGAAGAGATTTCCCTTCGTATCATATTTTAT	855
Db	541	ATGGAACACACTGATGAATCAAAAGGGTGTAGTGAAGATTTTCCGAAATACCATTTTCAT	600
QY	856	CAACATCGTTTGGAAAAAGACTTACCTATGAAGACGGGGGTTCGTGAACAGCATATGAGACT	915
Db	601	CAACATCGTTTATGAGAAAGACTGATGTGGAAGACGGAGGTTTGTGAGCAACACGAGACG	660
QY	916	GCTATTTGCTCAATGACATCTATATGAAAAACCACTAGATCTTTACACGAATGGGTTTAA	975
Db	661	GCGATTTGCTCAACGACATCTCTTGGCAAAACCACTTTGATCTTTACACGAATGGGTTTAA	720

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RESULT 2
US-10-060-857-3
Sequence 3, Application US/10060857
Patent No. US2002013318A1
GENERAL INFORMATION:
APPLICANT: Anticancer, Inc.
APPLICANT: Zhao, Ming
APPLICANT: Jiang, Ping
APPLICANT: Xu, Mingxu
APPLICANT: Yang, Meng
TITLE OF INVENTION: IMPROVED FLORESCENT PROTEINS
FILE REFERENCE: 31276-20032.00
CURRENT APPLICATION NUMBER: US/10/060,857
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: US 60/264,932
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 720
TYPE: DNA
ORGANISM: Saccharomyces cerevisiae
US-10-060-857-3

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Query Match	42.9%	Score 462.4	DB 12	Length 720
Best Local Similarity	78.1%	Pred. No. 1.4e-94		
Matches 556: Conservative	0	Mismatches 156:	Indels 0	Gaps 0

[illegible]

OY	384	CGGCAATCAACTGGTTCAGATTCGTGTCACGAAAGGGGCCCACTGCTTCATTGGA	443
Db	129	TGGTAATCAATGGTCTCAAAATTAAGATTACAAAGGGTCCATGGCATTCCTTTTGA	188
OY	444	TATTGTGTCAACACCTTTTTCANATATGGCAACCCACTTCTTACGAAATATCCGAATATAT	503
Db	189	TATTTTGTCTCCAGCTTTTTCATATATGTAATATAGAACCTTTTACTTAATATTCACAAATAT	248
OY	504	ATCAGATTTATTTTATACATCATTTCCAGCAGCATTTTATCTATATGACGAATTTACGTTA	563
Db	249	TTTTCGATTTTTTATTCAAATCTTTTCCAGCTGGTTTTGTTATGAAAGAACTTTTGAGATA	308
OY	564	CGAGATGGGGGCACTTGTGAAATTCGTTCAGATATTAATTTAATATGAACACAAAGTTCCG	623
Db	309	TGAAGATGGTGCTTTGGTGTGAAATTAATCTGATATTTAATTTGATATGACAAATATGTTTG	368
OY	624	CTACAGATGTCATATACAAAGCTAGTAACCTCCAGATGATGGTCCGTCATCGCAGAAAC	683
Db	369	TTATATGAACTTAAATATTAAGGTACAAATTTTCCAAATGATGGTCCAGTTATGAAAAAAC	428
OY	684	TATCTTACGAATAGAGCCTTCATTGTAAGCCATCTACATGAATTAATGCGCTCTTGGTCGG	743
Db	429	TATTACTGCTTTCGACACCATCTTTTGAAGTTGTTTATATGAATGATGCTTTTGGTTGG	488
OY	744	CGAGATTAATTTCTGTCTATAACTTAACTCGGGAATATTTATTCATGTCACTGAACAC	803
Db	489	TCAAGTTTATTTTGGTTTATATACATTTGAATTCGTGTAATTTTATCTTGTCTATATGAGAAC	548
OY	804	ATTATATGAAGTCGAAGCTGTAGTAAGAGATTTCTCTTCGATACATTTTATCAACATCG	863
Db	549	TTTTCATGAATCTTAAGGTGTGTTGTAAGATTTTCCAGAAATATCATTTTATTTCAACATAG	608
OY	864	TTTGGAAAAAGACTTACGTAGAGAAGCGGGGCTTCGTTGAACAGCATGAGACTCTATTTGC	923
Db	609	ATTGGAAAAAACCATTATGTGTGAAGATGGTGTCTTTGTTGAACAACATGAACCTCTATTTGC	668
OY	924	TCAATATGACATCTATAGCAAAACCATAGCATCTTCAACGAAATGGGTTTAA	975
Db	669	TCAATATGACCTTTGGGTATACCATTTGGGTTCTTTCGATGAAATGGGTTTAA	720

RESULT 3
 US-10-060-857-4
 Sequence 4, Application US/10060857
 Patent No. US2002013318A1
 GENERAL INFORMATION:
 APPLICANT: AntiCancer, Inc.
 APPLICANT: Zhao, Ming
 APPLICANT: Jiang, Ping
 APPLICANT: Xu, Mingxu
 APPLICANT: Yang, Meng
 TITLE OF INVENTION: IMPROVED FLUORESCENT PROTEINS
 FILE REFERENCE: 31276-20032.00
 CURRENT FILING DATE: US/10/060.857
 CURRENT APPLICATION NUMBER: 2002-01-29
 PRIOR APPLICATION NUMBER: US 60/264,932
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 720
 TYPE: DNA
 ORGANISM: Escherichia coli
 US-10-060-857-4

Query Match	36.2%	Score	390.4	DB	12	Length	720
Best Local Similarity	71.4%	Pred. No.	1.8e-78				
Matches	514	Conservative	0	Mismatches	206	Indels	0
						Gaps	0

QY 256 AAGATGACCTAAACAATAATTATTTGAAGAACCCTTTCGTTTACAGAAGTAATCTCGTATATAAGTA 315,
| | | | | | | | | | | | | | | | | | | | | |
Db 1 ATGGTGAGCAACACAGATTCTGTAAAAAACCCGCCCTGCAGGAATTTATGACTTTTAAAGTC 60

QY	316	AACCTGGAAGCAATTGTAAACCAACCATCTTTTTCACATGAGAGGCTTGCGCAAAAGCAAT	375
Db	61	AACTCGGAAGCGCTGGCTGAACACCACTGTGTTTATCCATATGGAAGGCTTGCGCAAAAGGCAAC	120
QY	376	ATTATTTCGGGCATCAACTGGTTTCAGATTGCTGCACGAAGGGGCCCACTGCTCTT	435
Db	121	ATTCTGTTTGGCAACCACTGGTGCACATTGGCTGACCAAAAGCGCGCCCTTCCTTT	180
QY	436	GCATTGATATTGTGTACACAGCTTTTTCATATGGCAACCGTACTTTACGAAATATCCG	495
Db	181	GGCTTGTGATTTCTAGCCCCCGCTTTCAGATTGCAACCGCACCTTTACCAATAATATCCC	240
QY	456	AATGATATATCAGATATATTATTTATACAAATCATTTCCACAGAGATTATGATGAAGACA	555
Db	241	GAAGATATTACCGATTTTTTTATTACAGACTTTTCCCGGGCTTTGTGTATGAACGCACC	300
QY	556	TTACGTTACGAAGATGCGGCACTTGTTGAAATTCGTTTCAGATATAATTAATAGAAGAC	615
Db	301	CTGGCTTATGTAAGATGCGGCGCTCTGTTGAAATTCGCGACATATTAACCTGATTGAAGAA	360
QY	616	AAGTTCGCTCTCAGAGTCGATATACAAAGTAGTACTTCCACAGATGATGGTCCGTCATG	675
Db	361	ATGTTTGTCTATCCCTGGATATATAAGGCCCACTTTTCCACAGATGGCCCCGTGATG	420
QY	676	CAGAAGACTATCTTAGCAATAGAGCCTTCATTGTAAGCCCATCTACATGAATAATGGCTC	735
Db	421	AAAAAACCATTTACCGGCGCTGCACGCCACGCTTGAAGTGGTGATATGAACGATGGGGTG	480
QY	736	TTGCTGCGCGGAAGTATTTCTGTCTATAACTAAACCTCTGGGAATATTAATTATGTAC	795
Db	481	CTTGGGGGCCAGAGTATTTGTGTATCGCCTGAAACGGCGCAAAATTTTACTCTGCAT	540
QY	796	ATCAAAACATTTAATCAAGTCTCAAAAGGTGTAGTAAGAGATTTCTCCTCGTATCAATTTAT	855
Db	541	ATCGGCACCTCGATGAAACCAAGGGCGTGTGAAAGATTTTCCCGATATCATTTTATT	600
QY	856	CAACATCTTTTGGAAAGACCTTACGTAGAAAGAGCGGGGTTTCGTTGACAGCATGAGACT	915
Db	601	CAGCATCCCGCGGAAAAAACCTATGTGGAAGATGCGCGCTTTGTGGAAACAGCATGAAC	650
QY	916	GCTATTCTCAATACACATCTATAGAAAAACCACTAGATCTCTACAGCATGGTTTA	975
Db	661	CGCATTCGCGAGCTGACACAGCGCTTGGCAAAACCCCTGGCGACGCTGCATGATGGTGTA	720
RESULT 4			
US-10-060-857-5			
: Sequence 5, Application US/10060857			
: Patent No. US20020132318A1			
: GENERAL INFORMATION:			
: APPLICANT: AntiCancer, Inc.			
: APPLICANT: Zhao, Ming			
: APPLICANT: Jiang, Ping			
: APPLICANT: Xu, Mingxu			
: APPLICANT: Yang, Meng			
: TITLE OF INVENTION: IMPROVED FLUORESCENT PROTEINS			
: FILE REFERENCE: 31276-20032.00			
: CURRENT APPLICATION NUMBER: US/10/060.857			
: CURRENT FILING DATE: 2002-01-29			
: PRIOR APPLICATION NUMBER: US 60/264,932			
: NUMBER OF SEQ ID NOS: 9			
: SOFTWARE: FastSeq for Windows Version 4.0			
: SEQ ID NO 5			
: LENGTH: 720			
: TYPE: DNA			
: ORGANISM: Bifidobacterium longum			
US-10-060-857-5			

Query Match	34.1%	Score 368;	DB 12;	Length 720;
Best Local Similarity	69.48;	Pred. No. 1.8e-73;		
Matches 500;	Conservative 0;	Mismatches 220;	Indels 0;	Gaps 0

OY	236	AAGATGACTAAACAAATATTAGAGACACTTGTTTACAGAAGTAATGTCTATAAAGTA	3135
Db	1	ATGGTGCTCCAAAGACAGATCCTTAAAGAACCCGGCCTCGAGAGATCATGTCTCTTCAAGTGG	60
OY	316	AATCTGGAAGCAATGTGTAAACACCATGTTTTTCAATGTGAGGCTTCCGGCAAGGGCAAT	3757
Db	61	AACCTGGAGAGGGCGTGTGTAAACACCACGTGTTCAACATGGAGGGCTCGCGCAAGGGCAAC	1200
OY	376	AATTTTATTTCCGCAATCAACTGTTTCAGATTTCGTGCAGAAAGGGGCCCACTGCGCTTTT	4355
Db	121	ATCCGTGTTCCGCAACCAACACTGTGTAGATTCGGCTGTGACCAAGGGCGCGCTCCGCTTC	1800
OY	436	GCATTTCGATTTTGGTCCACAGCTTTTCAATATGGAACCGTACTTTTACGAATATTCGC	4959
Db	181	GCCTTCGCATCTCTGTCCCGGCTTCAGATGACGCAACCGACCTTCACCAACTACCGC	2400
OY	436	AATGATATATCAGATTATTTTATACAAATCAATTCACACAGAGATTTATGTATGAACGACA	5555
Db	241	GAGCGACATCTCCGACTTCTTCATCCAGCTCTTCCCGCGGCTTCGTGTAGACCGCACCC	3000
OY	556	TTACGTTTACGAAGATGGCGGCACTGTTCGAATTTCCGTTCAGATATAAATTTAATGAAAC	6151
Db	301	CTCGCTTACGAGAGACGGGGCCTGTGTGAGATTCGCTCCGACATCAACTGATCAGAGAG	3600
OY	616	AAGTTTCGTCTACAGAGTTCGAATACAAAGGTGTAACTTCCAGATGTAGTGGTCCCGTATG	6759
Db	361	ATGTTCTGTGTACCGGTGTGATACAAAGGCCCAACTTCCGACAGACAGCGCCGTATG	4200
OY	676	CAGAAGACTATCTTAGCAATAGACCTTCATTTGAAGCCATGTACATGAATATGGCGTC	7355
Db	421	AAGAAGACATCACCGGCTCCACCGCTCTTCGAGGTGTGTATCATGAACGACAGGGCGTG	4800
OY	736	TTGGTCGCGCAAGTAATCTTGTTATTAATCAACTGTGGAAATATTTATTCATGTAC	7859
Db	481	CTGGTGGGCCAAGTGATCCTGTGTACCGCTCGAATCTCGGCAAGTTCTACTCTCGCAC	5400
OY	736	ATGAAACATTAAATGAGTGAAGGTGTACTAAAGAGTTTCTCTTGATCATTTTATTT	8555
Db	541	ATCGCACCCCTGATGAATCTCCACGGCCTGTGTGAAGGACTTCCCGGAGTACACTTCATC	6000
OY	856	CAACATCGTTTGGAAAAACACTTACGTAGAAGACGGGGGCTTCGTGAACAGCATGACACT	9151
Db	601	CAGACACGCCCTGTGAAGAACTACTGTGAGAGACGGCGCTTCGTGTGAGACGACAGAGACC	6600
OY	916	GCTATTCTCAATGACATCTATAGGAAAAACCACTAGATCTTTACAGAAATGGGTTTAA	9755
Db	661	GCCATTCGCCACGCTACCTCTCTGGGCAAGCCGCTGGGCTCCCTGCACAGATGGGTGTAA	7200

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RESULT 5
US-09-795-040A-3
: Sequence 3, Application US/09795040A
: Patent No. US20020064842A1
: GENERAL INFORMATION:
: APPLICANT: Stratagene
: TITLE OF INVENTION: Renilla Reniformis Green Fluorescent Protein and Mutants There
: FILE REFERENCE: 25436/1162
: CURRENT APPLICATION NUMBER: US/09/795,040A
: PRIOR FILING DATE: 2001-02-26
: PRIOR APPLICATION NUMBER: US 60/185,589
: PRIOR FILING DATE: 2000-02-28
: PRIOR APPLICATION NUMBER: 60/210,561
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 3
: LENGTH: 720
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Humanized DNA
: NAME/key: exon
: LOCATION: (1)..(720)

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; OTHER INFORMATION: open reading frame
US-09-795-040A-3

Query Match
  31.1%; Score 336; DB 10; Length 720;
Best Local Similarity 66.7%; Pred. No. 2.6e-66;
Matches 480; Conservative 0; Mismatches 240; Indels 0; Gaps 0;

OY 256 AAGATGAGTAACCAATATTGGAAGACACTTGTGTACAGAAAGTAATGTCGTATTAAGTA 315
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Db 1 ATGTGTAGGACAGAGATCTCTGAAGAACACCGGCTCGAGAGATCATGAGCTTCAAGTGC 60

OY 316 AATCTGGAAGGAATTGTAAACAACCATGTTTTTACAAATGAGGGGTTGCGGCAAGGGAAT 375
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 AACCTGGAGGGCGTGGTGAACAACACGCTTCCATGACATGAGAGGGCTGCGGCAAGGGCAAC 120

OY 376 ATTTTATTCGGCAATCACTGTTGATTCGTGTACAGCAAGGGGCCCCACAGCTTTT 435
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 ATCTGTTCGGCAACACGCTGTTGATTCGTGTACAGCAAGGGGCCCCACAGCTTTT 180

OY 436 GCATTTGATATTGTGTACACGCTTTTCAATATGACACGCTTCTTCAAGAAATATCCG 495
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 GCCTTGACATCCTTGAGCCCGGCTTCCAATAGGCAACCGCACTTCCACCAAGTACCC 240

OY 496 AATGATATATCAGATTATTTTATCAATCATTTTCCAGCAGAGATTATGTATGAAGACA 555
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 GAGGACATCAGGCACTTCTTCAATCCAGAGCTTCCCGCGGCTTCTGTACAGAGCCACC 300

OY 556 TTACGTTAGCAAGATGGCGGCACTTGTGAATTCGTTCAAGATTAATTAATTAAGAAGAC 615
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 CTGCGCTACGAGAGCGGCGGCTGTGGAGATCCGACACCATCAACCTGATCGAGAG 360

OY 616 AAGTTGCTACAGAGTGCATATCAAAAGTAGTAACTTCCAGATGATGGTCCCGTCATG 675
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 ATGTTGCTGACCGCGTGAGATCAAGGGGCCCACTTCCCAACGAGCGGCCCGGATG 420

OY 676 CAGAACATATCTTAGAATAGACCTTCATTGGAAGCAATGTACATGAATATGGCGTC 735
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 421 AAGAAAGACATCACCGCGCTGACGCCAGCTTCGAGGTGTGTACATGAAGCAGCGGCTG 480

OY 736 TTGCTGGCGAAGTAATTTCTTGTCTATTAACCTAAGCTTGGGAATATTTATGATGTCAC 795
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 481 CTGTGGGCGGAGTGATCTCTGCTGTACCGGCTTAACAAGCGGCAAGTTCTACAGCTGCCAC 540

OY 796 ATGAAAAACATTAATGAAGTGAAGAGGTGTAGTAAAGAGATTCTTCGTATCATTTTAT 855
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 541 ATCCGACACCTGTATGAAGACAAAGGCGGTGTGAAGACTTCCCGAGTACCACTTCATC 600

OY 856 CAACATCGTTTGGAAAGACTTACGTAGAAGACGGGGGTTGTTGAACAGCATGAGACT 915
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 601 CAGACCGGCTGGAGAAGACTTACGTGAGAGACGGCGCTTCTGTGAGCAGCAGAGACC 660

OY 916 GCTATTGCTCAATGACATCTATAGAAAAACCACTAGACTCTTACAGCAATGGTTTAA 975
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 661 GCCATCGCCAGCTGACACAGCTTGGGCAAGCCCTTGGGAGGCTTGCACGAGTGGGTAA 720

RESULT 6
US-10-060-857-2
; Sequence 2, Application US/10060857
; Patent No. US20020132318A1
; GENERAL INFORMATION:
; APPLICANT: Anticancer, Inc.
; APPLICANT: Zhao, Ming
; APPLICANT: Jlang, Ping
; APPLICANT: Xu, Mingxu
; APPLICANT: Yang, Meng
; TITLE OF INVENTION: IMPROVED FLUORESCENT PROTEINS
; FILE REFERENCE: 31276-20032.00
; CURRENT APPLICATION NUMBER: US/10/060,857
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: US 60/264,932
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 9
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; SOFTWARE: FastSDQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Renilla reniformis
US-10-060-857-2

Query Match
  31.1%; Score 336; DB 12; Length 720;
Best Local Similarity 66.7%; Pred. No. 2.6e-66;
Matches 480; Conservative 0; Mismatches 240; Indels 0; Gaps 0;

OY 256 AAGATGAGTAACCAATATTGGAAGACACTTGTTCACAAGAACTAATGTCTTAAGTA 315
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ATGTGTAGGACAGAGATCTCTGAAGAACACCGGCTCGAGAGATCATGAGCTTCAAGTGC 60

OY 316 AATCTGGAAGGAATTGTAAACAACCATGTTTTTACAAATGAGGGGTTGCGGCAAGGGAAT 375
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 AACCTGGAGGGCGTGGTGAACAACACGCTTCCATGACATGAGAGGGCTGCGGCAAGGGCAAC 120

OY 376 ATTTTATTCGGCAATCACTGTTGATTCGTGTACAGCAAGGGGCCCCACAGCTTTT 435
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 ATCTGTTCGGCAACACGCTGTTGATTCGTGTACAGCAAGGGGCCCCACAGCTTTT 180

OY 436 GCATTTGATATTGTGTACACGCTTTTCAATATGCAACCGTACTTTCACGAAATATCCG 495
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 GCCTTGACATCCTTGAGCCCGGCTTCCAATAGGCAACCGCACTTTCACCAAGTACCC 240

OY 496 AATGATATATCAGATTATTTTATCAATCATTTTCCAGCAGAGATTATGTATGAAGACA 555
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 GAGGACATCAGGCACTTCTTCAATCCAGAGCTTCCCGCGGCTTCTGTACAGAGCCACC 300

OY 556 TTACGTTAGCAAGATGGCGGCACTTGTGAATTCGTTCAAGATTAATTAATTAAGAAGAC 615
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 CTGCGCTACGAGAGCGGCGGCTGTGGAGATCCGACAGCATCAACCTGATCGAGAG 360

OY 616 AAGTTGCTACAGAGTGCATATCAAAAGTAGTAACTTCCAGATGATGGTCCCGTCATG 675
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 ATGTTGCTGACCGCGTGAGATCAAGGGGCCGCACTTCCCAACGAGCGGCCCGGATG 420

OY 676 CAGAACATATCTTAGAATAGAGCTTCATTTGGAAGCAATGTACATGAATATGGCGTC 735
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 421 AAGAAAGACATCACCGGCTGACGCCAGCTTCGAGGTGTGTACATGAAGCAGCGGCTG 480

OY 736 TTGCTGGCGAAGTAATTTCTTGTCTATTAACCTAAGCTTGGGAATATTTATGATGTCAC 795
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 481 CTGTGGGCGGAGTGATCTCTGCTGTACCGGCTTAACAAGCGGCAAGTTCTACAGCTGCCAC 540

OY 796 ATGAAAAACATTAATGAAGTGAAGAGGTGTAGTAAAGAGATTCTTCGTATCATTTTAT 855
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 541 ATCCGACACCTGTATGAAGACAAAGGCGGTGTGAAGACTTCCCGAGTACCACTTCATC 600

OY 856 CAACATCGTTTGGAAAGACTTACGTAGAAGACGGGGGTTGTTGAACAGCATGAGACT 915
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 601 CAGACCGGCTGGAGAAGACTTACGTGAGAGACGGCGCTTCTGTGAGCAGCAGAGACC 660

OY 916 GCTATTGCTCAATGACATCTATAGAAAAACCACTAGACTCTTACAGCAATGGTTTAA 975
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 661 GCCATCGCCAGCTGACACAGCTTGGGCAAGCCCTTGGGAGGCTTGCACGAGTGGGTAA 720

RESULT 7
US-09-977-897-1
; Sequence 1, Application US/09977897
; Publication No. US2002019763A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Yin-Tai
; APPLICANT: Cao, Longguang
; TITLE OF INVENTION: A synthetic DNA encoding an orange seapen-derived green fluore
; FILE REFERENCE: 41856-5
; CURRENT APPLICATION NUMBER: US/09/977,897
; CURRENT FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 27
```

```

: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1
: LENGTH: 1482
: TYPE: DNA
: ORGANISM: Ptilosarcus gurneyi
: US-09-977-897-1
```

```

Query Match      27.2% Score 294; DB 9; Length 1482;
Best Local Similarity 63.7%; Pred. No. 7.7e-57;
Matches 447; Conservative 0; Mismatches 253; Indels 0; Gaps 0;
```

```

OY 275 TGAAGAACACTTGTTCACAGAAAGTAATGCTATTAAGTAATCTGGAGAAATTGTAA 334
    |||||
DB 32 TGAAGAACACGGCGCTGAAGAGATCATGACGCCCAAGGCCAGCGTGGAGGACATGCTGA 91

OY 335 ACAACCATGTTTACATGAGAGGTTCCGGCAAGGGAATATTTATTTGCGAATCAAC 394
    |||||
DB 92 ACAACCAACGCTTCACATGAGAGGCTTCGGCAAGGCCAACGTCGTCTGCGCAACCAAC 151

OY 395 TGGTTGAGATTGCTGTCAGCAAGGGGCCACAGCCCTTTGATTTGATTTGTTGTGAC 454
    |||||
DB 152 TGAATGAGATCGGGGTGACCAAGGGCGGCCCTCTGCCCTTCGACATGCTGAGCA 211

OY 455 CACCTTTTCATATGGCAACCGTACTTTTCAGAAATATCCGAATGATATTCAGATTAT 514
    |||||
DB 212 TCCCTTCAGTACGGCAACCGGACCTTCACAAAGTATCCCGAGACATGCGCGACTACT 271

OY 515 TTATACATTCATTTCAGCAGAGATTATGATACCAACATTAACCTTACGAAGATGGCG 574
    |||||
DB 272 TCTTGAGAGACCTTCCTCGCGGCTTCTTACAGCGCAACCTCGCTTCGAGACGCGG 331

OY 575 GACTTTGTAATTCGTTGATATTAATTAATAGAACAGTTCGTTGATGAGAGTTCG 634
    |||||
DB 332 GCATGCTGACATCCGGAGGACATCAAGCTTGAGAGCAAGCAAGTTCCATCTACAGTGG 391

OY 635 AATACAAAGGTAGTAACCTCCAGATGATGGTCCGTCATGACAGAAAGTACTTTAGAA 694
    |||||
DB 392 AGTACCGCGGCAACGGCTTCCTAGCAAGCGCCCTTGATGCAAGAGCCATCCTGGGCA 451

OY 695 TACAGCCTTCATTGAAAGCATGATGATATGAGCGCTTGGTGGGGAAGTAAATTC 754
    |||||
DB 452 TGAGAGCCAGCTTCGAGGTGGTGTACATGAACAGCGCGCTGCTGGGAGGTGGACC 511

OY 755 TTGCTATTAACATAACTGTGGAATAATATTATTCATGTCACATGAAGCAATTAATGAGT 814
    |||||
DB 512 TGGTGTACAAAGCTGAGAGAGGCGCACTACTACAGCTGCCAATGAGACCTTCTACCGCA 571

OY 815 CGAAGCTGTAGTAAAGAGCTTTCCTGTATCATTTTATTAACATGCTTTGGAAGA 874
    |||||
DB 572 GCAAGCGCGCGTGAAGAGATTCCTGTAGTACCTATTCATCCACGACCGGCTGGAGAGA 631

OY 875 CTTAGCTAAGAGAGCGGGGTTGCTTGACAGATGAGACTGCTATTTGCTCAATGACAT 934
    |||||
DB 632 ACTACGTGAGAGGAGGAGCTTCGTGGAGAGCAGACAGACCGGCACTGCGACGTGCA 691

OY 935 CTATAGCAAAACCACTAGAGATCCTTACAGCAATGCGTTTAAA 976
    |||||
DB 692 CCATGCGCAAGGCTCTGGCGAGCCTGCAGCAGTGGGTGTTAAA 733

RESULT 8
US-09-967-772-7
: Sequence 7, Application US/09967772
: Patent No. US20020164577A1
: GENERAL INFORMATION:
: APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
: APPLICANT: TSIEN, Roger
: APPLICANT: GONZALEZ, Jesus
: TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY OPTICAL METHODS
: FILE REFERENCE: REG1290-5
: CURRENT APPLICATION NUMBER: US/09/967,772
: CURRENT FILING DATE: 2001-09-28
: PRIORITY APPLICATION NUMBER: US 09/459,956
```

```

: PRIOR FILING DATE: 1999-12-13
: PRIOR APPLICATION NUMBER: US 08/765,860
: PRIOR FILING DATE: 1996-12-19
: PRIOR APPLICATION NUMBER: PCT/ US96/09652
: PRIOR FILING DATE: 1996-06-06
: PRIOR APPLICATION NUMBER: US 08/481,977
: PRIOR FILING DATE: 1995-06-07
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 7
: LENGTH: 801
: TYPE: DNA
: ORGANISM: Clavularia sp
: US-09-967-772-7
```

```

Query Match      15.0% Score 161.4; DB 9; Length 801;
Best Local Similarity 56.1%; Pred. No. 2.8e-27;
Matches 325; Conservative 0; Mismatches 251; Indels 3; Gaps 1;
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```

OY 293 AAGAGTAATGTCGTATTAAGTAATCTGAGAGGAATTTGTAACCAACCATGTTTACAA 352
    |||||
DB 140 ACCCAGACATGAAGATTAACTGAAGATGGAAGAAATGTAAACGGGCACTGTTGTGA 199

OY 353 TGGAGGTTGCGGCAAGGGAATATTTTATTTCGCAATCAACTGTTTCAGATTGCTGCA 412
    |||||
DB 200 TCGAGAGAGAGAGAGAGGAAGCAAGCTTACATGGGACACACTTTAACTGGAAGTGA 259

OY 413 CGAAGGGGCGCCAGCTGCTTTGATTTGATATTTGTGTGACAGCACTTTCAATATGCA 472
    |||||
DB 260 AGAAGGTGCGGCTTCCTTTTCTTACGATATCTTCAACGGCGTTCAGACAGAA 319

OY 473 ACCGTACTTCAGGAATATCCGAATGATATATCAGATTTTATATCATCATTTCCAG 532
    |||||
DB 320 ACAGAGCATTTGACAAATPACCCAGACATATPACAGACTATTTCAAGCAAGTCTTCCG 379

OY 533 CAGATTTATGTAATGAAGCAACATTACGTTACGAAAGATGCGGCACTTGTGAATTCGTT 592
    |||||
DB 380 AGGATATTTCTTGGAAGAAAGCAACCATGACTTTTGAAGCAAAAGCATTTGTAAGTGA 439

OY 593 CAGATTAATTTAATAGAAGACAGTTCGCTACAGAGTGCATTAACAAAGTATGACT 652
    |||||
DB 440 GTGACATTAACATGAGAGAGACTCCTTTATATGAATTCCTTTGATGGGATGAACT 499

OY 653 TCCACAGATGATGTCGCCGTCATGACAGAGACTATTCATGAAGAAAGCCCTCAATTGAAG 712
    |||||
DB 500 TTCTCCCAATGATGCGGTATATGCAAAAAAATTGAAAGTGGGAACCATCCACTGAGA 559

OY 713 CCATGTACATGAATTAATGCGCTTGTGCGGCAAGTAAATTTGCTATAAATTAACACT 772
    |||||
DB 560 TTATGTAGTCGTGCGTGAAGAGTCTGTGTCGACATATTTACCATTTCTCTGCTGGAGG 619

OY 773 CTGGGAATATTAATTCATGTCACATGAGAAACATTAATGAAGTGAAGGTAGTAAAG 832
    |||||
DB 620 GAGGTGCGCATTCACCATGTGACTTCAAAAGTATTTACAAAGCAAAAAAAGGTGTCA --- 676

OY 833 AGTTTCTTGTATCATTTTATTCATCAATGCTTTGGA 871
    |||||
DB 677 AATTGCCAGACTATCACTTTGTGGACCATGCAATTGAGA 715

RESULT 9
US-10-066-922-3
: Sequence 3, Application US/10006922
: Publication No. US20020197676A1
: GENERAL INFORMATION:
: APPLICANT: Lukyanov, Sergey A
: APPLICANT: Fradkov, Arcady F.
: APPLICANT: Labas, Yulii A.
: APPLICANT: Matz, Mikhail V.
: APPLICANT: Tersikh, Alexey
: TITLE OF INVENTION: No. US20020197676A1el Chromophores/fluorophores and
: TITLE OF INVENTION: Methods for using the same
: FILE REFERENCE: CLON-035CIP
```



```
OY 745 GAAGTAATCTTGCTGATATAAATACTGGAATATTTATTCATGTCATGAATAACA 804
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 519 GACATCATCATCTGCTGCACAGTGGAGAGGTGCTCATACGTATTCATTAATAACT 578
OY 805 TTAATCAAGTCGAAGAGTGTAGTAAGAGCTTTCCTTCATCATTTTATTCACATCGT 864
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 579 GTTTACAGGCGCAAGAAGCCCGTAAGATCCAGGCTATCATACTGTGACCAACTCG 638
OY 865 TTGCAAAACACTTACGTAGACAGCGGGGCTGTTGACAGCATGAGACTGCTATTGCT 924
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 639 GTTATAGGAGCAGACCAAGAAATTCATGAAGTTGAGAGCATGAATCGCGTTGCA 698
OY 925 C 925
    |
Db 699 C 699
```

```
RESULT 11
US-09-967-772-5
: Sequence 5, Application US/09967772
: Patent No. US20020164577A1
: GENERAL INFORMATION:
: APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
: APPLICANT: TSIEN, Roger
: APPLICANT: GONZALEZ, Jesus
: TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY OPTICAL METHODS
: FILE REFERENCE: REGEN1290-5
: CURRENT APPLICATION NUMBER: US/09/967,772
: CURRENT FILING DATE: 2001-09-28
: PRIOR APPLICATION NUMBER: US 09/459,956
: PRIOR FILING DATE: 1999-12-13
: PRIOR APPLICATION NUMBER: US 08/765,860
: PRIOR FILING DATE: 1996-12-15
: PRIOR APPLICATION NUMBER: PCT / US96/09652
: PRIOR FILING DATE: 1996-06-06
: PRIOR APPLICATION NUMBER: US 08/481,977
: PRIOR FILING DATE: 1995-06-07
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 5
: LENGTH: 699
: TYPE: DNA
: ORGANISM: Discosoma striata
US-09-967-772-5
```

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Query Match 12.8% Score 138.5; DB 9; Length 699;
Best Local Similarity 51.9% Pred. No. 3.3e-22;
Matches 337; Conservative 0; Mismatches 309; Indels 3; Gaps 1;
```

```
OY 280 AACACTTGTTTACAGACGTAATGCTATTAAGTAATCTGGAAGCAATTGTAACAC 339
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 13 AAGAGTGTCATCAGCAACAATAATGTTGATCGATCTTCATCTGGAAAGACGTTCAATGG 72
OY 340 CATGTTTTCACATGAGAGGCTTCGGCAAGCAATATTTTATTCGCAATCAACTGTT 399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 73 CACTACTTTGAATAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAATACCGT 132
OY 400 CAGATTTCGTGTCAGCAAGAGGCGCCGCTTTTCATTTGATATTTGTCACAGCT 459
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 133 ACGCTGACGTTACCAAGGCTGACCTTCGCCATATTTTGTGCCACAA 192
OY 450 TTTCATATGCGCAACGCTACTTTACGAATATCCGAATGATATATCAATATTTTATA 519
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 193 TTTCAGTATGGAAGCAAGCAATTTTGTCCACACCCCTGCAACACTACATATATTTAAAG 252
OY 520 CAATCAATTTCCAGACGATTTATGTATGAAGCAACATTACGTTACGAAGATGGCGACTT 579
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 253 CTGTCAATTTCCGAGAGATATACATGTGGAACGCTCCATCTTGAACAGCGTGGCTTG 312
OY 580 GTTGAATTCGTTGAGATTAATTTAATGAAGCAAGTTCGCTACGAGCTCGAATAC 639
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 313 TGTTCATACCAATGATATGAGTTTGACAGCAACTGTTTCTACTACGACATCAAGTTC 372
```

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OY 640 AAAGTAGTACTTCCAGATGATGTCGCCGTCATGACAGACGATCTTACGAATAGAG 699
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 373 ACGGCTTGACATTTCTCCCAATATGACCCGCTGTGCAAGAAAGCAACATGGCTGGAA 432
OY 700 CTTTCATTTCAAGCCATGACATGAATATGAGCTTGTGGCGCAAGTAACTTTGTC 759
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 433 CCGAGCACTGAGGTTTGTATCTCGTGAATGCTGTGTTGATAGAGACATCATATGCT 492
OY 760 TATTAACATAACTCTGGGAATATTTATCATGTCACATGAATAACATTATGAAGTGA 819
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 493 CTGACAGTTGCAAGAGGTGCTCATTCGATGACATGATGAATAAATCTTTACAGGGCCA 552
OY 820 GGTGTAGTAAGAGGTTTCTTCATCATTTATTTCA--ACATCGTTTGAAGAACT 876
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 553 AAGCGCCCTTGAAGATGCCAGGTATCTACTATGTCACCAACTGTTATATGGAAC 612
OY 877 TACGTAGACAGCGGGGCTTCGTTGAACAGCATGAGCTGCTATGCTC 925
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 613 AAGCAACAAGAAATTCATGAAGTTGAGAGCATGAATGCGCGCTGCAC 661
```

```
RESULT 12
US-09-967-772-6
: Sequence 6, Application US/09967772
: Patent No. US20020164577A1
: GENERAL INFORMATION:
: APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
: APPLICANT: TSIEN, Roger
: APPLICANT: GONZALEZ, Jesus
: TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY OPTICAL METHODS
: FILE REFERENCE: REGEN1290-5
: CURRENT APPLICATION NUMBER: US/09/967,772
: CURRENT FILING DATE: 2001-09-28
: PRIOR APPLICATION NUMBER: US 09/459,956
: PRIOR FILING DATE: 1999-12-13
: PRIOR APPLICATION NUMBER: US 08/765,860
: PRIOR FILING DATE: 1996-12-15
: PRIOR APPLICATION NUMBER: PCT / US96/09652
: PRIOR FILING DATE: 1996-06-06
: PRIOR APPLICATION NUMBER: US 08/481,977
: PRIOR FILING DATE: 1995-06-07
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 6
: LENGTH: 678
: TYPE: DNA
: ORGANISM: Discosoma sp "red"
US-09-967-772-6
```

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Query Match 12.5% Score 134.8; DB 9; Length 678;
Best Local Similarity 50.8% Pred. No. 2.3e-21;
Matches 322; Conservative 0; Mismatches 312; Indels 0; Gaps 0;
```

```
OY 280 AACACTTGTTTACAGACGTAATGCTATTAAGTAATCTGGAAGCAATTGTAACAC 339
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 13 AAGATGTTATCAGAGAGTTCATGAGCTTTAAGCTTCGATGGAAGCAAGCGTCAATGG 72
OY 340 CATGTTTTCACATGAGAGGCTTCGGCAAGCAATATTTTATTCGCAATCAACTGTT 399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 73 CAGAGTATTGAATFAGAAAGCGAAGAGAGAGGAGGCCATAGCAAGGCCCAATACCGTA 132
OY 400 CAGATTTCGTGTCAGCAAGAGGCGCCGCTTTTCATTTGATATTTGTCACAGCT 459
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 73 CAGAGTATTGAATFAGAAAGCGAAGAGAGAGGAGGCCATAGCAAGGCCCAATACCGTA 132
OY 450 TTTCATATGCGCAACGCTACTTTACGAATATCCGAATGATATATCAATATTTTATA 519
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 193 TTTCAGTATGGAAGCAAGATATATGTCAAGCAACCCCTGCCAGACATACCACTATATAAAG 252
OY 520 CAATCAATTTCCAGACGATTTATGTATGAAGCAACATTACGTTACGAAGATGGCGACTT 579
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 253 CTGTCAATTTCCGAGAGATTTAATATGGAAGAGGTCATGAACCTTTGAAGACGCTGGCTG 312
```


QY	400	CAGATTCCTGTCACGAAGAAGGGCCCACTGCCCTTTGCATTGATTTGGTCTACACAGCT	459
Db	186	AAGCTTAAGGTAAACCAAGGGGGACCTTTGGCATTTCCTTGGATTAATTTTGTCAACCAAA	2435
QY	450	TTTCAATATGGCAACCGGTACTTTTCAGCAAAATATCCGATATGATATATGATTCATTTATATA	519
Db	246	TTTTCAGTATGCAAGCAAGGTATATGTCAGACACCTCCGACATACGACACTATAAAG	3059
QY	520	CAATCATTTTCAGCAGCAATTTATGTAAGCAACAACTTACGTTAGCAAGATGGCGACTT	579
Db	306	CTGTGATTTCTCGAAGGATTTAAATGGGAAGGGTCTGTAACCTTTGAAGACGGGTGGCTC	3659
QY	580	GTTGAATTCCTTCGATATATTAATTTAAATGAAACAGGTCCCTCTACAGCTCGAATAC	639
Db	366	GTTACTGTAAACCCAGACTTCAGTTTTCAGAGATGCGCTGTTTCACTACAAAGGTACATTC	4259
QY	640	AAAGTAGTAACTTCCAGATGATGTCGCCGTATGCAAGACATTACTTAGCAATAGAG	699
Db	426	ATTTGGCGTGAACCTTCCCTTCGATGAGACCTGTTATGCAAAAAGAACAAATGGCTGGAA	485
QY	700	CCTTTCATTGAAGCCATGTCATGATCAATTAATGGCTTTGGTCGGCAAGTAATTCCTTGTG	759
Db	486	GCCAGCACTGAGCCCTTGATACCTCGATGATGGCTGTGAAGAGAGATTCATTAAGCT	5459
QY	760	TATAACTAACTCTGGGAATATTATTACATGTCACATGAAACATTAAATGAACTGAAA	819
Db	546	CTGAAGCTGAAGAAAGCGGGTCTATTACCTAGTTGAATTCGAATTAATTAATTCATGGCAAG	605
QY	820	GGGTAGTAAAGGAGTTTCCCTCTTCATCATTTTATTCACATCGTTTGGAAAGACTTAC	879
Db	606	AAGCCTGTCCAGCTACGACGAGGTACTACTACTGTTGACTCCCAACTGGATATAACCAAGCCAC	6655
QY	880	GTAGACAGCGGGGGCTTCGTTGAACAGCATGAGA	913
Db	666	AACGACACTATACAACTGTTGACAGCATGAGAA	599

RESULT 15

US-09-976-673-3

; Sequence 3, Application US/09976673

; Patent No. US20020160473A1

; GENERAL INFORMATION:

; APPLICANT: Lukyanov, Sergey

; APPLICANT: Pradkov, Arcady

; APPLICANT: Labas, Yulii

; APPLICANT: Matz, Mikhail

; APPLICANT: Lukyanov, Konstantin

; APPLICANT: Gurskaya, Nadezda

; TITLE OF INVENTION: FAR RED SHIFTED FLUORESCENT PROTEINS

; FILE REFERENCE: CLON-028WO

; CURRENT APPLICATION NUMBER: US/09/976,673

; PRIOR FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/240,018

; PRIOR FILING DATE: 2000-10-12

; PRIOR APPLICATION NUMBER: 60,306,131

; PRIOR FILING DATE: 2001-07-16

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 908

; TYPE: DNA

; ORGANISM: heteractis crispa

; US-09-976-673-3

Db	145	TTTTCAGTGTGAAGGACGAGGAGCGGCAACCCATTACAGCTACGGAGACATGAGCAT	204
QY	405	TGCTGCACGAAMGGGGCCCATCGCCCTTTGGCATTTGATATGTTGCACACAGCTTTTCA	464
Db	205	TGATGTCAACGAAGGGCGTCATTACCATTTGGCTTCGACATTTTGGCACCCTGTTGTGA	264
QY	465	ATATGGCAACCGTACTTTTCACGAATATCCGATGATATACGATTTATTTTATACATC	524
Db	265	GTACGGCAGACGAGACCTTTGTCCACCATACGGCAGAGATTCGCCATTTCTTCAACGAGTC	324
QY	525	ATTTCACAGCAGATTTATGTAATGTAAGCAACATTAAGTTACGTAAGATGGCGACTTTGTGA	584
Db	325	TTTCCCTGAAGCCTTTACTCTGGGAAGAACACACCACTGATGAAGATGGAGCATTTCTTAC	384
QY	585	AATTTCGTTCAGATATTAATATTTAATAGAAGACAGTGTGCTACAGATCGATATCAAAAG	644
Db	385	TGTCATCATGAGCACCAAGACCTGGAGGGGAACCTGCTTATATACAGCTGGAAGACCTCTTG	444
QY	645	TAGTAACCTGCCAATATGATGTGTCCCGTCATGCACAAAGACATATCTTAGGAATAGAGCTTC	704
Db	445	TACCAATTTTCTCTCTGATGAGCCCGGTGATGAAGAACAAATACAGAAAGATGGGAGCATG	504
QY	705	ATTGGAAGCCATGACATGAATTAATGGCGCTTGCTGGG	743
Db	505	CACGTAGGTGCTTTATCCAGATTAATGCTGCTCTGTGG	543

Search completed: January 16, 2003, 15:01:49
Job time : 68.8186 secs

	Query Match	12.3%	Score 132.6	DB 5	Length 908
	Best Local Similarity	55.6%	Pred. No. 7,9e+21		
	Matches 255	Conservative 0	Mismatches 204	Indels 0	Gaps 0
QY	285	TTGTTTACCAAGACGTAATGCTCTATTAACTAAATCTGCAAGCAATTTGTAAACACCATGT	344		
Db	85	TTTGTTCAAGAAACATATGGCGCATCAAGATGTACATCGAAGGCACCGTTTAAATGGCCATTAA	144		
OY	345	TTTAAACAATGCAAGCGCTTCCGCCCAAGGCAATATTTTATTGGCAATCAACGTGGTTCAGAT	404		

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 16, 2003, 11:04:35 ; Search time 3016.15 Seconds

(without alignments)
10652.486 Million cell updates/sec

Title: US-09-710-058A-3

Perfect score: 1104
Sequence: 1 tcggcagcagcgcgcctcca.....caaaaaaaaaaaaaaaaaa 1104

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl :
1: gb_ba : *
2: gb_hlg : *
3: gb_id : *
4: gb_om : *
5: gb_ov : *
6: gb_pat : *
7: gb_ph : *
8: gb_pl : *
9: gb_pr : *
10: gb_ro : *
11: gb_sts : *
12: gb_sy : *
13: gb_un : *
14: gb_vi : *
15: em_ba : *
16: em_fun : *
17: em_hum : *
18: em_in : *
19: em_mu : *
20: em_om : *
21: em_or : *
22: em_ov : *
23: em_pat : *
24: em_ph : *
25: em_pl : *
26: em_ro : *
27: em_sts : *
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29: em_vi : *
30: em_hlg_hum : *
31: em_hlg_inv : *
32: em_hlg_other : *
33: em_hlg_mus : *
34: em_hlg_pln : *
35: em_hlg_rtd : *
36: em_hlg_mam : *
37: em_hlg_vrt : *
38: em_sy : *
39: em_hlgo_hum : *
40: em_hlgo_mus : *
41: em_hlgo_other : *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1104	100.0	1104	6	AR151735 Sequence
2	1104	100.0	1104	6	AX146237 Sequence
3	1104	100.0	1104	6	AX250588 Sequence
4	1094	99.1	1094	3	AY015595 Ptiliosarc
5	760.2	68.9	1279	6	AR151735 Sequence
6	760.2	68.9	1279	6	AX146238 Sequence
7	760.2	68.9	1279	6	AX250589 Sequence
8	394.2	35.7	1066	3	AY015996 Renilla m
9	394.2	35.7	1079	6	AX250573 Sequence
10	394.2	35.7	1085	6	AR151730 Sequence
11	392.6	35.6	1079	6	AX146235 Sequence
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13	257.8	23.4	860	6	AX250582 Sequence
14	256.2	23.2	864	3	AF372525 Renilla r
15	256.2	23.2	864	6	AX250581 Sequence
16	256.2	23.2	873	6	AX250583 Sequence
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19	160	14.5	801	6	AX172855 Sequence
20	160	14.5	801	6	AX207716 Sequence
21	160	14.5	801	6	AX233582 Sequence
22	160	14.5	1116	3	AF168424 Clavulari
23	145.2	13.2	845	3	AF420591 Dendronop
24	137.8	12.5	795	3	AY037770 Montastr
25	135.8	12.3	1178	3	AY037767 Scolymia
26	133.4	12.1	681	6	AX233584 Sequence
27	133.4	12.1	713	6	AX233627 Sequence
28	132.4	12.0	666	6	AX348043 Sequence
29	132.4	12.0	666	6	AX353910 Sequence
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34	132.4	12.0	859	3	AF168419 Discosma
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39	132.2	12.0	699	6	AX207714 Sequence
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42	132	12.0	687	3	AF322221 Anemona
43	131.4	11.9	955	3	AF246709 Anemona
44	130.2	11.8	1030	3	AY037765 Agaricia
45	129.8	11.8	699	3	AF322222 Anemona

ALIGNMENTS

RESULT 1
LOCUS AR151735 1104 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 30 from patent US 6232107.
ACCESSION AR151735
VERSION AR151735.1 GI:15117785
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 1104)
Bryan, B.J. and Szent-Gyorgyi, C.
Luciferases, fluorescent proteins and the use thereof in
diagnostics, high throughput screening and novelty items

QY 481 TTGAGGTGCTACATGAACACGGCGTTCTGCTGGCGAAGTAGATCTGTTACAAA 540
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Db 481 TTTCAGGTGCTACATGAACACGGCGTTCTGCTGGCGAAGTAGATCTGTTACAAA 540
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Db 541 CTCGACTCAGGACTATTACTGCTGCCACATGAAACGTTTACAGATCCAAAGTGGCA 600
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Db 1081 TGATCAAAAAAAAAAAAAAAAA 1104

RESULT 3
AX250588 1104 bp DNA linear PAT 05-OCT-2001
LOCUS AX250588
DEFINITION Sequence 30 from Patent WO0168824.
ACCESSION AX250588
VERSION AX250588.1 GI:15984339
KEYWORDS
SOURCE
ORGANISM
Ptiliosarcus gurneyi.
Ptiliosarcus gurneyi.
Eukaryota; Metazoa; Chordata; Anthozoa; Alcyonaria; Pennatulacea;
Subellipsozoa; Pennatulidae; Ptiliosarcus.
1 (bases 1 to 1104)
Bryan, B.J., Szent-Gyorgyi, C. and Szecepaniak, W.
Renilla reniformis fluorescent proteins, nucleic acids encoding the
fluorescent proteins and the use thereof in diagnostics, high
throughput screening and novelty items
Patent: WO 0168824-A 30 20-SEP-2001;
Protime, Ltd. (US); Bryan, Bruce J. (US)
FEATURES
source
Location/Qualifiers
1..1104
/organism="Ptiliosarcus gurneyi"
/db_xref="taxon:161601"
34..750
/note="Ptiliosarcus Green Fluorescent Protein"
/codon_start=1
/protein_id="CAC93791.1"
/db_xref="GI:15984340"

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BASE COUNT 360 a 215 c 237 g 292 t
ORIGIN

Query Match 100.0%; Score 1104; DB 6; Length 1104;
Best Local Similarity 100.0%; Pred. No. 2.6e-257;
Matches 1104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 GGACTGAAAGACATTATGTCGGCAAAAGCTAGCGTTGAAGGAATCGTGAACATTCAGTT 120
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QY	961	ATTAAACGGCTTTCACACGACAGTGGAACTCTTTAAACCGATCAAACTATTATTAAT	1020
Db	961	ATTAAACGGCTTTCACACGACAGTGGAACTCTTTAAACCGATCAAACTATTATTAAT	1020
QY	1021	ATATATACCGCTGTAACTTATATATATATATATATAGTTTGGATATGATTAACTGTTCT	1080
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QY	1081	TGATCAAAAAAAAAAAAAAAAAAAAA 1104	
Db	1081	TGATCAAAAAAAAAAAAAAAAAAAAA 1104	
RESULT 4			
LOCUS	AY015995	1094 bp	mRNA linear INV 15-JUN-2001
DEFINITION	Ptiliosarcus sp. CSG-2001 green fluorescent protein (GFP) mRNA,		
ACCESSION	AY015995		
VERSION	AY015995.1		
KEYWORDS	GI:12621057		
SOURCE	Ptiliosarcus sp. CSG-2001.		
ORGANISM	Eukaryota; Metazoa; Chordata; Anthozoa; Alcyonaria; Pennatulacea;		
REFERENCE	1 (bases 1 to 1094)		
AUTHORS	Szent-Gyorgyi,C.S. and Bryan,B.J.		
TITLE	Luciferases and fluorescent proteins, nucleic acids encoding the		
JOURNAL	diagnosics, high throughput screening and novel items		
REFERENCE	2 (bases 1 to 1094)		
AUTHORS	Szent-Gyorgyi,C.S. and Bryan,B.J.		
TITLE	Direct Submission		
JOURNAL	Submitted (07-DEC-2000) Prolume Ltd., 1085 William Pitt way,		
FEATURES	Pittsburgh, PA 15238, USA		
source	Location/Qualifiers		
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	/db_xref="GI:12621058"		
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ORIGIN			
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Best Local Similarity	100.0%; Pred. No. 6,8e-255;		
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QY	11	CTGGCCTCCACACTTTAGACAAATGAACCGACAGTATTAAAGACACTGACGTGAAG 70	
Db	1	CTGGCCTCCACACTTTAGACAAATGAACCGACAGTATTAAAGACACTGACGTGAAG 60	
QY	71	AGATTATGTGCGCAAAAGCTACGCTTGAAGGAATGCTGAACAATACAGCTTTTTCATGG 130	
Db	61	AGATTATGTGCGCAAAAGCTACGCTTGAAGGAATGCTGAACAATACAGCTTTTTCATGG 120	

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Db	121	AAGGATTTGGAAAAAGGCATGATATATTTGGAAACCAATTCAGTCAAAATCCGGGTTACAA	180				
OY	191	AAGGAGTCCTGGTCCATTCCTCTTCATATGTTTCCATAGCTTCCAAATACGGGAATC	250				
Db	181	AAGGAGTCCTGGTCCATTCCTCTTCATATGTTTCCATAGCTTCCAAATACGGGAATC	240				
OY	251	GCATTTTCACGAATAATACCAGACGACATTCGCGACTCTTGTTCATATTCCTCCGCTG	310				
Db	241	GCATTTTCACGAATAATACCAGACGACATTCGCGACTCTTGTTCATATTCCTCCGCTG	300				
OY	311	GATTTTTCACGAAGAANTCAGCCTTGGAAAGTGGCGCATTTGTACAAATTCGTTACG	370				
Db	301	GATTTTTCACGAAGAANTCAGCCTTGGAAAGTGGCGCATTTGTACAAATTCGTTACG	360				
OY	371	ATATAGATTGTAGAAAGATGATAAATTCCACTACAAAGTGGAGTATAGAGCAACGGTTTC	430				
Db	361	ATATAGATTGTAGAAAGATGATAAATTCCACTACAAAGTGGAGTATAGAGCAACGGTTTC	420				
OY	431	CTAGTAAACGGACCCGTGATGCAAAAAAGCCATCCTCGCATGGAGCCATCGTTTGAGTTGG	490				
Db	421	CTAGTAAACGGACCCGTGATGCAAAAAAGCCATCCTCGCATGGAGCCATCGTTTGAGTTGG	480				
OY	491	TCTACATGACACAGCGCGCTTCTGCTGGCGCGAAGTATGATCTCGTTTACAAACTCCAGTACG	550				
Db	481	TCTACATGACACACCGCGCTTCTGCTGGCGCGAAGTATGATCTCGTTTACAAACTCCAGTACG	540				
OY	551	GGAATCTATTACCTCGGCCACATGAAAGCTTTTACAGATCCAAAGCTGGAGTGAAGAAT	610				
Db	541	GGAATCTATTACCTCGGCCACATGAAAGCTTTTACAGATCCAAAGCTGGAGTGAAGAAT	600				
OY	611	TCCCGGAATATTCATTTATCCATCATCGTCTGGAGAAAAACCTACGTGGAAGAAGAACT	670				
Db	601	TCCCGGAATATTCATTTATCCATCATCGTCTGGAGAAAAACCTACGTGGAAGAAGAACT	660				
OY	671	TCTGTGGAACACACGACGAGCGCATTTGCACAACTATCCACAATTTGGAAAACCTCTGGGCT	730				
Db	661	TCTGTGGAACACACGACGAGCGCATTTGCACAACTATCCACAATTTGGAAAACCTCTGGGCT	720				
OY	731	CCCTTCATGAATGGGTGTAGAAATGACCAATATCTGGGGAGAACCGAATACCGTTTGA	790				
Db	721	CCCTTCATGAATGGGTGTAGAAATGACCAATATCTGGGGAGAACCGAATACCGTTTGA	780				
OY	791	AGCTGTGTATACAAATTAATTTGGGGTCATTTTGTAAATGTGTATGTGTGTATGATCA	850				
Db	781	AGCTGTGTATACAAATTAATTTGGGGTCATTTTGTAAATGTGTATGTGTGTATGATCA	840				
OY	851	ATAGACGTCGTATTCATATAGCTTTGAATCCTTCACGAAAAAAACCTCGAAGCATATTGAA	910				
Db	841	ATAGACGTCGTATTCATATAGCTTTGAATCCTTCACGAAAAAAACCTCGAAGCATATTGAA	900				
OY	911	ACCTGAAGCATATTTGAAACCTCGACGGGAGACCGTAAAGAGACCGCACAAATTAACGGGT	970				
Db	901	ACCTGAAGCATATTTGAAACCTCGACGGGAGACCGTAAAGAGACCGCACAAATTAACGGGT	960				
OY	971	TTTCAACACGACAGTGGAAATCTTTAAACCGATCAAAACTATTAAATTAATATATATATACCC	1030				
Db	961	TTTCAACACGACAGTGGAAATCTTTAAACCGATCAAAACTATTAAATTAATATATATATACCC	1020				
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Db	1021	TGTATTAATCTATATATATCTATATATAGTTGATATTTGAATTAATCTGTCTTGATCAAAA	1080				
OY	1091	AAAAAAAAAAAAAAAA 1104					
Db	1081	AAAAAAAAAAAAAAAA 1094					
RESULT 5							
AR151736							

ACCESSION AR151736
VERSION AR151736.1 GI:15117786
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1279)
AUTHORS Bryan, B.J. and Szent-Gyorgyi, C.
TITLE Luciferases, fluorescent proteins, nucleic acids encoding the
diagnostics, high throughput screening and the novelty items
JOURNAL Patent: US 6232107-A 31 15-MAY-2001;
FEATURES
source Location/Qualifiers
BASE COUNT 449 a 234 c 263 g 333 t
ORIGIN
Query Match 68.9% Score 760.2; DB 6; Length 1279;
Best Local Similarity 80.5%; Pred. No. 7.1e-174;
Matches 1026; Conservative 0; Mismatches 33; Indels 216; Gaps 3;
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DB 61 CCTAGCGTTGAAGGATGCGTGAACATCAAGCTTTTCATGAGAGATTGGAAGGC 120
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DB 181 TTGCGCTTGGATATGTTTTCATAGCTTTTCATAGCGGATTCGACGAAATAC 240
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QY 328 AATCTAGCGTTTGAAGATGGCGGCAATTTGTCATTTGTCAGATATAGTTTGAAGAT 387
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DB 421 ATGCAAAAGGCACTCTGGGCAATGAGCGCATGCTTGAGTGGTCTACATGAACAGCCGC 480
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QY 748 TAGAAAATGACCAATATCTGGGAAA----- 774
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RESULT 6
AX146238
LOCUS AX146238 1279 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 4 from Patent WO0134824.
ACCESSION AX146238
VERSION AX146238.1 GI:14284756
KEYWORDS
SOURCE Ptiliosarcus gurneyi.
ORGANISM Ptiliosarcus gurneyi
Eukaryota; Metazoa; Chnidaria; Anthozoa; Aleyonaria; Pennatulacea;
Subelliflorae; Pennatulidae; Ptiliosarcus.
REFERENCE 1. (bases 1 to 1279)
AUTHORS Anderson, D.
TITLE Methods and compositions comprising ren11a gfp
JOURNAL Patent: WO 0134824-A 4 17-MAY-2001;
Rigel Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
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/organism="Ptiliosarcus gurneyi"
/db_xref="taxon:161601"
7. 723
/note="unnamed protein product"
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BASE COUNT 449 a 234 c 263 g 333 t
ORIGIN
Query Match 68.9% Score 760.2; DB 6; Length 1279;
Best Local Similarity 80.5%; Pred. No. 7.1e-174;

Matches 1026; Conservative 0; Mismatches 33; Indels 216; Gaps 3;

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Oy 208 TTGCGCTTCGATATTTGTTCCATACGCTTCCATACGGGAATCGCACTTTCAGGAATATC 267
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Db 181 TTGCGCTTCGATATTTGTTCCATACGCTTCCATACGGGAATCGCACTTTCAGGAATATC 240
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Oy 328 AATCTACGCTTTGAAGATGCGCCCATTTGTTGACATTCGTTCAAGATATAAGTTAGAAGAT 387
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Db 301 AATCTACGCTTTGAAGATGCGCCCATTTGTTGACATTCGTTCAAGATATAAGTTAGAAGAT 360
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Oy 508 GTTCTGGTGGGGAAGTATCTCGTTTACAACCTCGAATCAGGACATTAATCTGCTGC 567
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Db 481 GTTCTGGTGGGGAAGTATCTCGTTTACAACCTCGAATCAGGACATTAATCTGCTGC 540
Oy 568 CACATGAAAACGTTTTTACAGATCCAAAGGTGAGTGAAGAAATTCGCCGAATATCACTTT 627
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Oy 748 TTGAATAATGACAATATCTGCGGAAA----- 774
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Oy 775 ----- 774
Db 841 TTACTGGGAAAATGACCAATTTACTGTAGAAAATCACCATATATCTGTGAAAATGACCA 900
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Oy 856 CGTGTGATTCATAGCTTAATCTTTCAGCAAAAAGAACCTCGAAGCATATTTGAACCTTC 915
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Oy 916 GAAGCATATTTGAACCTTCGACGAGCGCTAAGAGACCGCAAAATTAACGCTTTCAA 975
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Oy 1035 -----TAAGTTATATATATATATATAGTTTGAATGATTAATGCTTGTGATCAAAA 1089
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Oy 1090 AAAAAAAAAAAAAAAAAA 1104
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Db 1243 AAAAAAAAAAAAAAAAAA 1257

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RESULT 7
AX250589 1279 bp DNA Linear PAT 05-OCT-2001
LOCUS
DEFINITION Sequence 31 from Patent WO0168824.
ACCESSION AX250589
VERSION AX250589.1 GI:15984341
KEYWORDS
SOURCE
ORGANISM
Ptiliosarcus gunneyi.
Ptiliosarcus gunneyi.
Eukaryota; Metazoa; Chordata; Anthozoa; Alcyonaria; Pennatulacea;
Subellilliores; Pennatulidae; Ptiliosarcus.
1 (bases 1 to 1279)
REFERENCE
Bryan, B.J., Szent-Gyorgyi, C. and Szczepaniak, W.
Renilla reniformis fluorescent proteins, nucleic acids encoding the
fluorescent proteins and the use thereof in diagnostics, high
throughput screening and novelty items
Patent: WO 0168824-A 31 20-SEP-2001;
Location/Qualifiers
1..1279
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/db_xref="taxon:161601"
7..723
/note="Ptiliosarcus Green Fluorescent Protein (GFP)"

FEATURES
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BASE COUNT 449 a 234 c 263 g 333 t
ORIGIN

Query Match 68.9%; Score 760.2; DB 6; Length 1279;

Best Local Similarity 80.5%; Pred. No. 7.1e-174;

Matches 1026; Conservative 0; Mismatches 33; Indels 216; Gaps 3;

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Oy 28 GACAAATAACCGGACGACTATTAAAGAACTGACGTGAAGAGATATATGTCGGCAAA 87
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Oy 88 GCTACGCTTGAAGGAATGCTGACAACTGCTTTTCCATGGAAGGATTTGAAAAGGC 147
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Db 181 TTGCGCTTCGATATTTGTTCCATACGCTTCCATACGGGAATCGCACTTTCAGGAATATC 240

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QY	258	CCACACGCAATTCGGGACCTCTTGTCATCTACATTCGCCGCTGGATTTCCTACCAAGA	322
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QY	328	AATCTACGCTTTGAAGATGGCGCCATTGTTGACATTCGTTCCAGATTAAGTTTAAAGAT	387
Dp	301	AATCTACGCTTTGAAGATGGCGCCATTGTTGACATTCGTTCCAGATTAAGTTTAAAGAT	360
QY	388	GATTAAGTTCCACTACAAAGTGGAGTATAGAGGCACGCGTTTCCTAGTAACGGACCCGTG	447
Dp	361	GATTAAGTTCCACTACAAAGTGGAGTATAGAGGCACGCGTTTCCTAGTAACGGACCCGTG	420
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QY	568	CACATGAAAGGTTTTCACATCCAAAGGTGGGTGAAGCAATTCGCCGAATATACATT	627
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QY	628	ATTCATCATCCTCTGGAGAAACCTACGTCGAGAGAAAGCTTCGTGAMACACAGAG	687
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QY	688	ACGGCCATTTGCACACACTGACACAAATTTGCAAAACCTCTGGCTCCCTTCATGAATGGTG	747
Dp	661	ACGGCCATTTGCACACACTGACACAAATTTGCAAAACCTCTGGCTCCCTTCATGAATGGTG	720
QY	748	TAGAAATGACCAATTAATCTGCGGGAAA-----	774
Dp	721	TAGAAATGACCAATTAATCTGCGGGAAA-----	780
QY	775	-----	774
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QY	775	-----	774
Dp	841	TTACTCGGGAAATGACCATTCTACTGTAGAAATTCACCAATTAATCTGTGCAAAATGACCA	900
QY	775	-----CGATTAACCGTTTGAAGCTT	795
Dp	901	AAATACTGTAAGAAATCTTCACACTGGGTGATTACCGTTTCGATTAACGTTTGGAAAGCTT	960
QY	796	GTGATACCAATTAATTTGGGGCTCATTTTGTATGTGTATGTGCTGTTGATGATCAATAGA	855
Dp	561	GTGATACCAATTAATTTGGGGCTCATTTTGTATGTGTATGTGCTGTTGATGATCAATAGA	1020
QY	856	CGTGTATTTCATAGCTTGGATCTTCACAGAAAGAAACCTCGAAGCATAATTGAACCTGC	915
Dp	1021	CGTGTATTTCATAGCTTGGATCTTCACAGAAAGAAACCTCGAAGCATAATTGAACCTGC	1062
QY	916	GAACCATATTGAACCTCGACGAGAGCGGTAAAGACACGCAACAATTACGCGCTTGAA	975
Dp	1063	GAACCATATTGAACCTCGACGAGAGCGGTAAAGACACGCAACAATTATTAATTA	1122
QY	976	GCACCACTGGCAATCTTAAAGCGCATCAAAACGATTAATATATATATATATACCTGTGA-	1034
Dp	1123	GCACCACTGGCAATCTTAAAGCGCATCAAAACGATTAATATATATATATATACACCTGTATGA	1183
QY	1035	-----TAACTTATATATATCTATATATAGTTTGGATATGATTAATCTGTTCTGATCAAA	1089
Dp	1183	CATATATATATATATATATATCTACATAGTTTGAATATGATTAATCTGTTCTGATCACTA	1242
QY	1050	AAAAAAAAAAAAAAAA 1104	
Dp	1243	AAAAAAAAAAAAAAAA 1257	

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	gene	CDS
AY015996	Renilla muelleri green fluorescent protein (GFP) mRNA, complete cds.	AY015996	AY015996.1	GI:12621059	Renilla muelleri. Eukaryota; Metazoa; Cnidaria; Anthozoa; Aleyonaria; Pennatulacea; Sesiiliflorae; Renillidae; Renilla.	2 (bases 1 to 1066)	Szent-Gyorgyi, C.S. and Bryan, B.J.	Direct Submission Submitted (07-DEC-2000)	Promluene Ltd., 1085 William Pitt Way, Pittsburgh, PA 15238, USA	1. 1066 /organism="Renilla muelleri" /db_xref="taxon:37510"	1. 1066 /gene="GFP"	246..962 /gene="GFP"
327	AAATCTAGCGTTTGAAGATGGCGCATCTGTGACATTCGTCACATATAAGTTAAGAAG	386	539	AACATTACGTTACGAGATGGCGACTCTGTGAATATTCGTCAGATTAAATTTAATGACA	598							
27	AGACAAATGAAACCCGACGATTTAAACACACTGACGTAAGAGATTATGTCGGCAA	86	239	AGATAAGTAGTAAACAAATTTTGAACACACTGTTTACACAGAGTAATGTCTATATA	298							
87	AGCTAGCGTTGAAGAAATCGTAACAAATCAGGTTTTTTCATGGAAGATTTGGAAGA	146	299	AGTAATCTGGAAGAAATTTGAACACACATGTTTTCATCATGAGAGGTCGCGCAAGG	358							
147	CAATGATATTTTGGAAACCAATGATGCAATCCGGGTTACAAAGGAGAGTCCGTTCC	206	359	GAATATTTTATTTGGCAATCAACTGCTTCACATTCGTCACAGAAAGGCGCCCACTCC	418							
207	ATTGCTTTGATATTTGTTTCCATAGCTTTTCCAAATGCGGAATGCACTTTACAGAAATA	266	419	TTTTCGATTTGATATTTGTCACCGACTTTTCAATATGGAACCACTTTACAGAAATA	478							
267	CCCAGACGACATTTGCGGACTACTTTGTTCAATCATTTCCGGGCTGGATTTTCTAGAAAG	326	479	TCCGATGATATATACGATTTATTTTATACAAATCATTTCCACAGAGATTTATGTAAAGC	538							
327	AAATCTAGCGTTTGAAGATGGCGCATCTGTGACATTCGTCACATATAAGTTAAGAAG	386	539	AACATTACGTTACGAGATGGCGACTCTGTGAATATTCGTCAGATTAAATTTAATGACA	598							

[illegible]

RESULT 9	AX250573	1079 bp	linear	PAT 05-OCT-2001
LOCUS	AX250573			
DEFINITION	Sequence	15 from Patent WO0168824.		
ACCESSION	AX250573			
VERSION	AX250573.1	GI:15984321		
KEYWORDS				
SOURCE				
ORGANISM	<i>Renilla muelleri</i> . <i>Renilla muelleri</i> . Eukaryota; Metazoa; Cnidaria; Anthozoa; Alcyonaria; Pennatulacea; Sessiliflorae; Renillidae; <i>Renilla</i> . 1 (bases 1 to 1079) Bryan,B.J., Szent-Gyorgyi,C. and Szczepaniak,W. <i>Renilla</i> reniformis fluorescent proteins, nucleic acids encoding the fluorescent proteins and the use thereof in diagnostics, high throughput screening and novelty items Patent: WO 0168824-A 15 20-SEP-2001; Prolume, Ltd. (US) : Bryan, Bruce J. (US)			
FEATURES				
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CDS				
BASE COUNT	375 a	176 c	209 g	319 t
ORIGIN				

	Query Match	Similarity	Score	DB 6:	Length	1079;
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	Matches	519;	Conservative	0;	Mismatches	208; Indels 0; Gaps 0
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OY	87	AGCTAGCGTTTGAAAGCAT	TGTCAGACANTACACTTTTTCATTCATGGAAGCATTGGAAAAG	146		

Db	312	AGTAATCTCGAAGCAATTTCTTAACACACCATGTTTTTACATGGAGGGTTGGCGGCAAC	371
Qy	147	CAMTATATTATTATTTGGAAACCAATGTGATGCMAATCCGGGTATACAAAGGAGNGTCGTCC	206
Db	372	GAATATTATTATTTGGCAATCAACGTGTTACAGATTGTTGTCAGAAAGGGGCCCATCTCC	431
Qy	207	ATTGGCTTTGCATATTGTTTCCATAGCTTTCCAAATAGCGGAATCGCACCTTTTCAGAAATA	266
Db	433	TTTTTCATTATTGATTTGTTGTCCACGCTTTTCAATATGGAACCCCTACTTTCCACAAATA	491
Qy	267	CCACAGCGCATCTGGGCACTACTTGTTCATATCATTCGCCGGCTGGAATTTTCTACGAAG	326
Db	492	TCCGATGATATATCAGATTATTATTATACAAATCATTTCCAGAGGATTTATGTATGAACG	551
Qy	327	AAATTCAGCTTTGAAGATGGCGCATTTGTTGACATTTGTCAGATATATAGTTTGAAGA	386
Db	552	AACATTACGTTACGAAGATGGCGACCTTGTGAATTTGTTTCAGATATATAATTTTATATGA	611
Qy	387	TGATAGATTCCACTCAAAAGTGGACTATAGAGCGCAACGGTTCCCTACTAACGCAACCGT	446
Db	612	AGACAGATCTCGTCAACAGTGGAAATACAAAGGTAGTAACTTCCAGATGATAGTGGCCGT	671
Qy	447	GATGCAAAAAGCGATCCGTCGGCATGGAGCGATCGTTTGAGCGTGTCATGATGAACGCG	506
Db	672	CATGCAAGAAAGCTATCTTAGCAATAGAGCTTCAATTTGAAGCCATGTACATGAATAATGG	731
Qy	507	CGTTCTGGTGGGGAAGTAGATCTGTTTACAAATCGAGAGTGGGAACATTACTCGNG	566
Db	732	CGTCTTGGTCGGCGAAGTAATCTTGTCTATTAACATTAAACCTCGGGAATATTATTACATG	791
Qy	567	CCACATGAAGCGTTTTTACAGATCCAAAGGTGGAGTGAAGCAATTTCCCGAATATCACTT	626
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Qy	627	TATTCATCATCTCGTGGGAAGAAACCTACCTGGAGCAACGAACCTTCGTGGAAACACAGGA	686
Db	852	TATTTCAACATCTTTTGGAAAGACTTACGTAGAAACCGGGGGCTTCTGTGAACACATGA	911
Qy	687	GAAGCGCATTTGCACAACTGACCAACCAATTTGGAAACCTCTGGGCTCCCTTCATGAATGGGT	746
Db	912	GACGTCTATTGCTCAAAATGACATCTATAGAAACACACCTAGATCTCTTAACAGATGGGT	971
Qy	747	GTAGAAA 753	
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RESULT#	10				
LOCUS	AR151730				
DEFINITION	AR151730	1085 bp	DNA	linear	PAT 08-AUG-2001
ACCESSION	Sequence 15	from patent US 6232107.			
VERSION	AR151730				
KEYWORDS	AR151730.1	GI:15117780			
SOURCE	.				
ORGANISM	Unknown.				
REFERENCE	Unknown.				
AUTHORS	1 (bases 1 to 1085)				
TITLE	Bryan, B.J. and Szent-Gyorgyi, C.				
	luciferases, fluorescent proteins, nucleic acids encoding the				
	luciferases, and fluorescent proteins and the use thereof in				
	diagnostics, high throughput screening and novelty items				
JOURNAL	Patent: US 6232107-A	15 15-MAY-2001;			
FEATURES	Location/Qualifiers				
source	1..1085				

	BASE COUNT	376 a	176 c	209 g	320 t	4 others
ORIGIN						
Query Match	35.7%					
Best Local Similarity	71.4%					
Matches 519; Conservative	0; Mismatches 208; Indels 0; Gaps 0;					

LOCUS AF383623 9258 bp DNA circular SYN 19-JUN-2001
DEFINITION Cloning vector pREXILLC, complete sequence.
ACCESSION AF383623
VERSION AF383623.1 GI:14487946
KEYWORDS Cloning vector pREXILLC.
SOURCE Cloning vector pREXILLC.
ORGANISM artificial sequences: vectors.
REFERENCE 1 (bases 1 to 9258)
AUTHORS Murakawa, M. and Freeman, M.W.
TITLE Adeno-associated virus 2 (AAV)-based plasmid vector system that can mediate auto-excision of AAV terminal motifs via auto-regulated transient Rep78 expression
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 9258)
AUTHORS Murakawa, M. and Freeman, M.W.
TITLE Direct Submission
JOURNAL Submitted (18-MAY-2001) Lipid Metabolism Unit, Massachusetts General Hospital, Jackson 1328, Boston, MA 02114-2694, USA
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BASE COUNT 2108 a 2386 c 2604 g 2160 t
ORIGIN
Query Match 30.2% Score 333.2; DB 12; Length 9258;
Best local Similarity 66.0%; Pred. No. 3,5e-70;
Matches 482; Conservative 0; Mismatches 248; Indels 0; Gaps 0;
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RESULT 13
AX250582
LOCUS AX250582 860 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 24 from Patent WO0168824.
ACCESSION AX250582
VERSION AX250582.1 GI:15984331
KEYWORDS
SOURCE
ORGANISM Renilla reniformis.
Eukaryota; Metazoa; Cnidaria; Anthozoa; Alcyonaria; Pennatulacea;
Sessiliflorae; Renillidae; Renilla.
REFERENCE 1 (bases 1 to 860)
AUTHORS Bryan, B.J., Szent-Gyorgyi, C. and Szczepaniak, W.
TITLE Renilla reniformis fluorescent proteins, nucleic acids encoding the
fluorescent proteins and the use thereof in diagnostics, high
throughput screening and novelty items
Patent: WO 0168824-A 24 20-SEP-2001;
Proline, Ltd. (US); Bryan, Bruce J. (US)
JOURNAL Location/Qualifiers
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RESULT 14
AF372525 864 bp mRNA linear INV 15-JUN-2001
LOCUS AF372525
DEFINITION Renilla reniformis green fluorescent protein (GFP) mRNA, complete
CDS
AF372525.1 GI:14161474
SOURCE
ORGANISM Renilla reniformis.
Eukaryota; Metazoa; Cnidaria; Anthozoa; Alcyonaria; Pennatulacea;
Sessiliflorae; Renillidae; Renilla.
REFERENCE 1 (bases 1 to 864)
AUTHORS Szent-Gyorgyi, C.S. and Bryan, B.J.
TITLE Luciferases, fluorescent proteins, nucleic acids encoding the
luciferases and fluorescent proteins and the use thereof in
diagnostics, high throughput screening and novelty items
Patent: US 6232107-B 15-MAY-2001;
Proline Ltd.; 1085 William Pitt Way; Pittsburg, PA;
USA;

JOURNAL
REFERENCE 2 (bases 1 to 864)
AUTHORS Szent-Gyorgyi, C.S., Bryan, B.J. and Szczepaniak, W.
TITLE Direct Submission
JOURNAL Submitted (18-Apr-2001) Proline Ltd., 1085 William Pitt Way,
Pittsburg, PA 15238, USA
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Location/Qualifiers

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Best Local Similarity 61.9%   Pred. No. 1.4e-51;
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KEYWORDS
SOURCE
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            Eukaryota; Metazoa; Cnidaria; Anthozoa; Aleyonaria; Pennatulacea;
            Sessiliflorae; Renillidae; Renilla.
REFERENCE
AUTHORS    Bryan,B.J., Szent-Gyorgyi,C. and Szczepaniak,W.
TITLE       Renilla reniformis fluorescent proteins, nucleic acids encoding the
            fluorescent proteins and the use thereof in diagnostics, high
            throughput screening and novelty items
JOURNAL     Patent: WO 0168824-A 23 20-SEP-2001;
            Prolume, Ltd. (US); Bryan, Bruce J. (US)
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Best Local Similarity 61.9%   Pred. No. 1.4e-51;
Matches 424; Conservative 0; Mismatches 258; Indels 3; Gaps 1;
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GenCore version 5.1.3
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OM nucleic - nucleic search, using SW model

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

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5	760.2	68.9	1279	22	AAF89810	Nucleotide sequenc
6	760.2	68.9	1279	24	AAD22208	Ptilosarcus gurneyi
7	394.2	35.7	1079	20	AAZ27547	Renilla mulleri gr
8	394.2	35.7	1079	22	AAF89808	Nucleotide sequenc
9	394.2	35.7	1079	24	AAD22198	Renilla mulleri gr

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18	188	17.0	780	22	AA591380	Renilla reniformis
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27	139.2	12.6	681	24	ABA95906	Yeast optimised RF
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29	138.8	12.6	850	22	AAD03614	Discosoma striata
30	135	12.2	681	22	AAH47656	Anthozoon red fluo
31	134.6	12.2	910	24	ABK96464	cDNA fragment enco
32	133	12.0	962	24	AAI69491	A. sulcata asFP499
33	132.4	12.0	666	24	ABL61142	Red fluorescent pr
34	132.4	12.0	678	22	AAD13053	Discosoma sp. "red
35	132.4	12.0	678	22	AAD11142	Discosoma species
36	132.4	12.0	678	22	AAH47654	Discosoma sp. red
37	132.4	12.0	678	24	ABA95921	Yeast optimised RF
38	132.4	12.0	859	24	AAL47952	Discosoma red fluo
39	132.2	12.0	699	22	AAD13052	Discosoma striata
40	132.2	12.0	699	22	AAD11141	Discosoma striata
41	132.2	12.0	699	22	AAH47653	D. striata dsFP483
42	132.2	12.0	960	21	AA528682	Anemonia sulcata m
43	131.4	11.9	696	21	AA550884	Anemonia sulcata c
44	131.4	11.9	696	22	AAD03616	Anemonia sulcata c
45	131.4	11.9	955	21	AAA50883	Anemonia sulcata f

ALIGNMENTS

RESULT 1
ID AAZ27548 standard: DNA: 1104 BP.
AC AAZ27548;
XX
DT 13-DEC-1999 (first entry)
XX
DE Ptilosarcus green fluorescent protein coding sequence.
XX
XX Luciferase: green fluorescent protein; GFP; screening assay; diagnostics;
KW bioluminescence-generating system; toy; cosmetic; fairy dust; beverage;
KW body paint; squirt gun; balloon; slimy play material; soap; toothpaste;
KW ds.
XX
XX Ptilosarcus gurneyi.
XX
XX W09949019-A2.
XX
XX 30-SEP-1999.
XX
XX 26-MAR-1999; 99WO-US06698.
XX
XX 27-MAR-1998; 98US-0079624.
PR 15-JUN-1998; 98US-0089367.
PR 01-OCT-1998; 98US-0102939.
XX
PA (PROL-) PROLUME LTD.
XX (BRYA/) BRYAN B J.
XX
XX Bryan BJ, Szent-Gyorgyi C:
XX

DR WPI: 1999-580443/49.
DR P-PSDB: AAV39958.
XX New isolated Renilla mulleri, Gaussia and Pleuromamma luciferase and
PT Renilla and Ptilosarcus green fluorescent protein nucleic acids -
XX
XX
PS Claim 36; Page 230-231; 233pp; English.
XX
CC This sequence encodes a green fluorescent protein of the invention. The
CC invention relates to Renilla mulleri, Gaussia and Pleuromamma luciferase
CC and Renilla and Ptilosarcus green fluorescent protein (GFP) nucleic acids
CC and proteins. The luciferases and GFPs can be used in
CC bioluminescence-generating systems, assays, screening methods, diagnostic
CC method and articles of manufacture. They can be expressed using
CC e.g. bacterial, yeast, plant, insect or animal cells. The Renilla
CC mulleri, Gaussia and Pleuromamma luciferase or Renilla or Ptilosarcus
CC GFPs can be used in e.g. toys, cosmetics, fountain, personal care items,
CC fairy dust, beverages, soft drinks, foods, textile products, bubbles,
CC balloons, personal items, dentifrices, soaps, body paints, bubble bath,
CC ink or paper products. In particular, they can be used in e.g. squirt
CC guns, pellet guns, finger paints, foot bags, greeting cards, slimy play
CC material, clothing, bubble making toys, bath powders, cosmetics, body
CC lotions, gels, body powders, body creams, toothpastes, mouthwashes,
CC soaps, body paints, bubble bath, inks, wrapping paper, gelatins, icings,
CC frostings, greeting cards, beer, wine, champagne, soft drinks, ice cubes,
CC ice, dry ice or fountains. The nucleic acids can also be used to produce
CC transgenic fish and plants.
XX
SQ Sequence 1104 BP; 360 A; 215 C; 237 G; 292 T; 0 other:
Query Match 100.0%; Score 1104; DB 20; Length 1104;
Best Local Similarity 100.0%; Pred. No. 3.9e-259;
Matches 1104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 601 GTGAAAGATTCCCGGAATATCATCTTATCCATCGTCTGGAGAAAACTACCTGGAA 660
DB 601 GTGAAAGATTCCCGGAATATCATCTTATCCATCGTCTGGAGAAAACTACCTGGAA 660
QY 661 GAAGCAACCTTCGTGCAACACAGACAGCGCCATTGCAACAAGTACCACTAATGGAAAA 720
DB 661 GAAGCAACCTTCGTGCAACACAGACAGCGCCATTGCAACAAGTACCACTAATGGAAAA 720
QY 721 CCTCTGGGCTCCCTTCATGAATGGGTAGAAAATGACCAATATCTGGGGAACCGATA 780
DB 721 CCTCTGGGCTCCCTTCATGAATGGGTAGAAAATGACCAATATCTGGGGAACCGATA 780
QY 781 ACCGTTTGGACCTTGATACAAATTTATTTGGGGTCAATTTTGAATGTATGTGT 840
DB 781 ACCGTTTGGACCTTGATACAAATTTATTTGGGGTCAATTTTGAATGTATGTGT 840
QY 841 TGTATGATCAATAGACGTCGTATCATAGCTTGAATCTTCAGCAAAAAGAACTCGAA 900
DB 841 TGTATGATCAATAGACGTCGTATCATAGCTTGAATCTTCAGCAAAAAGAACTCGAA 900
QY 901 GCATATTGAAACCTCGAAGCATATTGAAACCTCGAAGAGAGAGCGTAAGAGACCGACAA 960
DB 901 GCATATTGAAACCTCGAAGCATATTGAAACCTCGAAGAGAGAGCGTAAGAGACCGACAA 960
QY 961 ATTAAAGCGCTTCAACACAGCAGCTTGGAAATCTTAAACGATCAAACTATTAATAAT 1020
DB 961 ATTAAAGCGCTTCAACACAGCAGCTTGGAAATCTTAAACGATCAAACTATTAATAAT 1020
QY 1021 ATATATACCTCTATPACTTATATATCTATATAGTTTGATATGATTAATCTGTCT 1080
DB 1021 ATATATACCTCTATPACTTATATATCTATATAGTTTGATATGATTAATCTGTCT 1080
QY 1081 TGATCAAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1104
DB 1081 TGATCAAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1104

RESULT 2
AAF89809
ID AAF89809 standard; DNA; 1104 BP.
XX
XX AAF89809;
AC XX
XX
DT 23-JUL-2001 (first entry)
XX
DE Nucleotide sequence of a green fluorescent protein.
XX
XX Retroviral vector; Renilla; green fluorescent protein; pgFP; rGFP; ss.
OS Ptilosarcus gurneyi.
XX
XX
FH key Location/Qualifiers
FT CDS 34..750
FT /*tag= a
FT /product= "green fluorescent protein (pgFP)"
PN W0200134824-A2.
XX
XX 17-MAY-2001.
PD
XX
XX 10-NOV-2000; 2000WO-US30915.
PF
XX
XX 10-NOV-1999; 99US-0164592.
PR
XX
XX (RIGI-) RIGEL PHARM INC.
PA
XX
XX
XX Anderson D;
PI
XX
XX WPI: 2001-329091/34.
XX
XX P-PSDB: AAB83916.
DR
XX
XX Novel retroviral vector, containing gene encoding Renilla green

PT fluorescent protein, useful as reporter for cell assays, particularly
 intracellular assays -

XX Example: Fig 3A; 83pp; English.

XX The specification describes a retroviral vector comprising a Renilla
 CC green fluorescent protein (pGFP or rGFP) gene. pGFP and rGFP proteins
 CC are useful as reporters for cell assays, particularly intracellular
 CC assays including methods of screening libraries using pGFP or rGFP, and
 CC for screening protein-protein, nucleic acid-protein or nucleic
 CC acid-nucleic acid interactions. pGFP or rGFP proteins are also useful
 CC in cellular assays, including assays for alterations in exocytosis,
 CC cell cycle regulation, apoptosis, cellular proliferation and/or
 CC differentiation. pGFP or rGFP proteins are also useful for elucidating
 CC bioactive agents that can cause a population of cells either to move
 CC out of one growth phase into another, or to arrest in a growth phase.
 CC pGFP or rGFP proteins are also useful for screening bioactive agents for
 CC their ability to modulate cell cycle regulation, including the activation
 CC or suppression of cell cycle checkpoint pathways and ameliorating
 CC checkpoint defects. The present sequence encodes pGFP.

XX Sequence 1104 BP; 360 A; 215 C; 237 G; 292 T; 0 other:

Query Match 100.0%; Score 1104; DB 22; Length 1104;
 Best Local Similarity 100.0%; Pred. No. 3.9e-259;
 Matches 1104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCGGCACGACGCTGGCTCCACACTTTAGACAAATGACCCGACACTATTAAAGAACT 60
 DB 1 TCGGCACGACGCTGGCTCCACACTTTAGACAAATGACCCGACACTATTAAAGAACT 60
 OY 61 GGACTGAAGACATTAATGCGCAAAAGCTAGCGTTGAAGAACTCGTGAACATCACGTT 120
 DB 61 GGACTGAAGACATTAATGCGCAAAAGCTAGCGTTGAAGAACTCGTGAACATCACGTT 120
 OY 121 TTTTCCATGGAAGATTTGGAAAAGCAATGTAATTTGGAACCAATTGATGCAATC 180
 DB 121 TTTTCCATGGAAGATTTGGAAAAGCAATGTAATTTGGAACCAATTGATGCAATC 180
 OY 181 CGGCTTACCAAGGAGGAGCTCGCTTCCATTCGTTGATATGTTTCATACGCTTCCAA 240
 DB 181 CGGCTTACCAAGGAGGAGCTCGCTTCCATTCGTTGATATGTTTCATACGCTTCCAA 240
 OY 241 TACGGCAATCGCACTTTACGAATATCCGAGACATTCGCGACTTTGTTCAATCA 300
 DB 241 TACGGCAATCGCACTTTACGAATATCCGAGACATTCGCGACTTTGTTCAATCA 300
 OY 301 TTCCCGGCTGATTTTTCAGCAAAAGAAATCTACGCTTTGAAGATGCGCAATTGTTGAC 360
 DB 301 TTCCCGGCTGATTTTTCAGCAAAAGAAATCTACGCTTTGAAGATGCGCAATTGTTGAC 360
 OY 361 ATTCGTTGATATAGTTTACGAATGATTAAGTTCCACTACAACTGAGATATAGAGCC 420
 DB 361 ATTCGTTGATATAGTTTACGAATGATTAAGTTCCACTACAACTGAGATATAGAGCC 420
 OY 421 AACGGTTTCCAGTAGACGACCCGATGATCAAAAAGCATCTCCGCAATGAGCCATCG 480
 DB 421 AACGGTTTCCAGTAGACGACCCGATGATCAAAAAGCATCTCCGCAATGAGCCATCG 480
 OY 481 TTTGAGTGGTCTACATGAACAGCGCGCTTCTGTTGGGAGAGTAGATTCGTTACAAA 540
 DB 481 TTTGAGTGGTCTACATGAACAGCGCGCTTCTGTTGGGAGAGTAGATTCGTTACAAA 540
 OY 541 CTCGAGTCAAGGAAGTATTACTGTCGCATGAAACGCTTTTACAGATCCAAAGGTGGA 600
 DB 541 CTCGAGTCAAGGAAGTATTACTGTCGCATGAAACGCTTTTACAGATCCAAAGGTGGA 600
 OY 601 GTGAAGAAGTATCCCGAATATACATTTATCGATCGTCTGGAGAAACCTACGTCGAA 660
 DB 601 GTGAAGAAGTATCCCGAATATACATTTATCGATCGTCTGGAGAAACCTACGTCGAA 660
 OY 661 GAAGGAAGCTTGTGGACACAGCAGAGCGCATTTGCAACACTGACCAATTTGGAAAA 720
 DB 661 GAAGGAAGCTTGTGGACACAGCAGAGCGCATTTGCAACACTGACCAATTTGGAAAA 720

DB 661 GAAGGAAGCTTGTGGACACAGCAGAGCGCATTTGCAACACTGACCAATTTGGAAAA 720
 OY 721 CCTCTGGGCTCCCTTCATGATGAGTGCTGTAAGAAATATACCAATATACTGGGAACCGATA 780
 DB 721 CCTCTGGGCTCCCTTCATGATGAGTGCTGTAAGAAATATACCAATATACTGGGAACCGATA 780
 OY 781 ACCGTTGGAGCTTGTGTATACAAATTTTGGGGTCATTTTGTAAATGATATGTCGT 840
 DB 781 ACCGTTGGAGCTTGTGTATACAAATTTTGGGGTCATTTTGTAAATGATATGTCGT 840
 OY 841 TGTATGATCAATAGACGCTGCTATCATATGCTTGAATCCCTTCAGCAAAAGCACTCGAA 900
 DB 841 TGTATGATCAATAGACGCTGCTATCATATGCTTGAATCCCTTCAGCAAAAGCACTCGAA 900
 OY 901 GCATATTGAAACCTCGACAGATATTGAACCTTCGACGAGAGCGTAAAGACCCGACAA 960
 DB 901 GCATATTGAAACCTCGACAGATATTGAACCTTCGACGAGAGCGTAAAGACCCGACAA 960
 OY 961 ATTAACGCGTTTCACACGAGTGGAAATCTTTAAACCGATCAAAACTATTATATTAAT 1020
 DB 961 ATTAACGCGTTTCACACGAGTGGAAATCTTTAAACCGATCAAAACTATTATTAAT 1020
 OY 1021 ATATATACCCCTGTATACCTTATATATATATATATATATATATATATATATATATAT 1080
 DB 1021 ATATATACCCCTGTATACCTTATATATATATATATATATATATATATATATATATAT 1080
 OY 1081 TGATCAAAAAAAAAAAAAAAAAAAAA 1104
 DB 1081 TGATCAAAAAAAAAAAAAAAAAAAAA 1104

RESULT 3
 AAD22207
 ID AAD22207 standard; DNA; 1104 BP.
 XX
 AC AAD22207;
 XX
 DT 12-FEB-2002 (first entry)
 XX
 DE Ptiliosarcus gunneyi green fluorescent protein encoding DNA #1.
 XX
 KW Green fluorescent protein; GFP; bioluminescence generating system; toy;
 KW Luciferase; finger paint; slimy play material; fishing lure; sparkler;
 KW doll; balloon; personal care item; cosmetic; bath powder; body cream;
 KW tooth paste; mouth wash; soap; body paint; ornamental transgenic plant;
 KW bubble bath; fountain; fairy dust; food; gelatin; icing; frosting; beer;
 KW wine; champagne; milk; soft drink; ice cube; ice; foot bag; beverage;
 KW dry ice; textile; clothing; paper product; greeting card; wrapping paper;
 KW ds.
 XX
 OS Ptiliosarcus gunneyi.
 XX
 FH Key Location/Qualifiers
 FT CDS 34..750
 FT /tag= a
 FT /product= "P. gunneyi green fluorescent protein"
 XX
 PN WO200168824-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 15-MAR-2001; 2001WO-US08277.
 XX
 PR 15-MAR-2000; 2000US-189651P.
 XX
 PA (PROL-) PROLUME LTD.
 PA (BRYA/) BRYAN B J.
 XX
 PI Bryan BJ, Szent-Gyorgyi C, Szczepaniak W;
 XX
 WP1; 2002-010561/01.
 DR P-PSDB; AAE13386.
 XX

PT Nucleic acids encoding Renilla reniformis green fluorescent proteins,
PT useful in diagnostic bioluminescence procedures -
XX
PS Disclosure: Page 172-173; 175pp; English.
XX

CC The patent discloses sea pansy (*Renilla reniformis*) green fluorescent
CC proteins (GFP) and their corresponding polynucleotides. The invention
CC also relates to sequences of the bioluminescence generating system
CC (e.g. Luciferase). *R. reniformis* GFP are used in diagnostic methods
CC and in the production of novelty items such as toys (e.g. squirt gun,
CC pellet gun, toy "Halloween" eggs, toy cigarettes, board/card game
CC toys), finger paints, slimy play material, bubbles in bubble making
CC toys, fishing lures, dolls, sparklers, magic wand toys, balloons,
CC personal care item (e.g. cosmetic, bath powders, body creams, tooth
CC pastes, mouth wash, soaps, body paints, bubble bath); ornamental
CC transgenic plants, fountain, fairy dust, food (gelatins, icings, ice,
CC frosting, beers, wine, champagne, milk, soft drinks, ice cubes, ice,
CC dry ice, beverage), textile (foot bag, clothing) and/or paper product
CC (greeting cards, wrapping paper). The present sequence is a DNA
CC encoding *Ptilosarcus gurneyi* green fluorescent protein.
XX

Sequence 1104 BP: 360 A: 215 C: 237 G: 292 T: 0 other:

Query Match 100.0%: Score 1104: DB 24: Length 1104:
Best Local Similarity 100.0%: Pred. No. 3.9e-259;
Matches 1104: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

```
OY 1 TCGGCACAGCTGGGCTCCACACTTTAGCAAAATGACCGGACGATTAAGAAGCACT 60
DB 1 TCGGCACAGCTGGGCTCCACACTTTAGCAAAATGACCGGACGATTAAGAAGCACT 60
OY 61 GCACGAAAGAGATTATGCGGCAAAAGCTAGCGTTGAAGAAATCGTGAACATCAGTT 120
DB 61 GCACGAAAGAGATTATGCGGCAAAAGCTAGCGTTGAAGAAATCGTGAACATCAGTT 120
OY 121 TTTTCCATGGAAGATTGGAAAAGGCAATGTAATTTGGAACCAATTGATGCAAAATC 180
DB 121 TTTTCCATGGAAGATTGGAAAAGGCAATGTAATTTGGAACCAATTGATGCAAAATC 180
OY 181 CGGGTTACAAAGGAGGTCGCTTGCATTCGCTTCGATTTGTTCCATCTACTTCCAA 240
DB 181 CGGGTTACAAAGGAGGTCGCTTGCATTCGCTTCCATCTACTTCCAA 240
OY 241 TACGGGAATCGCACTTTCAGAAATACCCAGAGCAATTCGCGACTACTTTGTCATCA 300
DB 241 TACGGGAATCGCACTTTCAGAAATACCCAGAGCAATTCGCGACTACTTTGTCATCA 300
OY 301 TTCCCGGCTGGATTTTTCAGCAAGAATCTACGCTTTGAAGATGGCCCATTTGTTGAC 360
DB 301 TTCCCGGCTGGATTTTTCAGCAAGAATCTACGCTTTGAAGATGGCCCATTTGTTGAC 360
OY 361 ATTGCTGATATAGTTAGTAAGATGATTAAGTTCCATACAAAGTGAGATAGAGGC 420
DB 361 ATTGCTGATATAGTTAGTAAGATGATTAAGTTCCATACAAAGTGAGATAGAGGC 420
OY 421 AACGGTTTCCCTAGTAACGAGCCCGTATGCAAAAAAGCCATCCTCGGCATGAGCCATCG 480
DB 421 AACGGTTTCCCTAGTAACGAGCCCGTATGCAAAAAAGCCATCCTCGGCATGAGCCATCG 480
OY 481 TTTTGAAGTGTCTACATGAACAGCGCGTTCTGTGGGGGAAGTAGATCTCGTTTCAAA 540
DB 481 TTTTGAAGTGTCTACATGAACAGCGCGTTCTGTGGGGGAAGTAGATCTCGTTTCAAA 540
OY 541 CTTCGAGTCAAGGAGATATACGTCGCCACATGAAGCTTTTACGATCCAAAGGTGGA 600
DB 541 CTTCGAGTCAAGGAGATATACGTCGCCACATGAAGCTTTTACGATCCAAAGGTGGA 600
OY 601 GTGAAGAATTTCCGGAATATCACTTATCCATCATCTGTGGAGAAACCTACGTGAAA 660
DB 601 GTGAAGAATTTCCGGAATATCACTTATCCATCATCTGTGGAGAAACCTACGTGAAA 660
OY 661 GAAGCAAGCTTCTGTGAACACAGACGAGCGCCATTGCAACAACCTGACCAATTTGAAAA 720
DB 661 GAAGCAAGCTTCTGTGAACACAGACGAGCGCCATTGCAACAACCTGACCAATTTGAAAA 720
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DB 661 GAAGCAAGCTTCTGTGAACACAGACGAGCGCCATTGCAACAACCTGACCAATTTGAAAA 720
OY 721 CCTGGGCTCCCTTCATGAATGGGTGTAGAAAAATGACCAATATACCTGGGAAACCGATA 780
DB 721 CCTGGGCTCCCTTCATGAATGGGTGTAGAAAAATGACCAATATACCTGGGAAACCGATA 780
OY 781 ACCGTTTGAAGCTTGTGTATACAAATTAATTTGGGCTCATTTTGTAAATGTATGTGT 840
DB 781 ACCGTTTGAAGCTTGTGTATACAAATTAATTTGGGCTCATTTTGTAAATGTATGTGT 840
OY 841 TGTATGATCATATAGACGTCGTCATTCATAGCTTGAATCTTCAGCAAAAAAGAACTCGCA 900
DB 841 TGTATGATCATATAGACGTCGTCATTCATAGCTTGAATCTTCAGCAAAAAAGAACTCGCA 900
OY 901 GCATTTTGAACCTCGAAGCATATTGAAAACCTCGACGAGACGCTTAAAGACGCGCACAA 960
DB 901 GCATTTTGAACCTCGAAGCATATTGAAAACCTCGACGAGACGCTTAAAGACGCGCACAA 960
OY 961 ATTAACGCGTTTCAACCAAGCACTTGGAATCTTTAAACCGATCAAAAGCTAATTAAT 1020
DB 961 ATTAACGCGTTTCAACCAAGCACTTGGAATCTTTAAACCGATCAAAAGCTAATTAAT 1020
OY 1021 ATATATACCTGTATATACCTTATATATATCTATATAGTTGATATGATTAATCTGTCT 1080
DB 1021 ATATATACCTGTATATACCTTATATATATCTATATAGTTGATATGATTAATCTGTCT 1080
OY 1081 TGATCAAAAAAAAAAAAAAAAAAAAA 1104
DB 1081 TGATCAAAAAAAAAAAAAAAAAAAAA 1104
```

RESULT 4
AAZ27549
ID AAZ27549 standard: DNA: 1279 BP.

XX AAZ27549:

DT 13-DEC-1999 (first entry)

DE Ptilosarcus green fluorescent protein coding sequence.

KW Luciferase: green fluorescent protein: GFP; screening assay; diagnosis;
KW bioluminescence generating system; toy; cosmetic; fairy dust; beverage;
KW body paint; squirt gun; balloon; slimy play material; soap; toothpaste;
XX ds.

OS Ptilosarcus gurneyi.

PN W09949019-A2.

PD 30-SEP-1999.

PE 26-MAR-1999; 99WO-0506698.

PR 27-MAR-1998; 98US-0079624.

PR 15-JUN-1998; 98US-0089367.

PR 01-OCT-1998; 98US-0102939.

PA (PROL-) PROLUME LTD.

PA (BRYA/) BRYAN B J.

PI Bryan BJ, Szent-Gyorgyi C;

DR WPI: 1999-580443/49.

DR P-PSDB: AAT39951.

PT New isolated *Renilla mulleri*, *Gaussia* and *Pleuromamma luciferase* and
PT *Renilla* and *Ptilosarcus* green fluorescent protein nucleic acids -
XX
PS Claim 36; Page 231-232; 233pp; English.

CC This sequence encodes a green fluorescent protein of the invention. The
CC invention relates to *Renilla mulleri*, *Gaussia* and *Pleuromamma luciferase*

CC and Renilla and Ptiliosarcus green fluorescent protein (GFP) nucleic acids
 CC and proteins. The luciferases and GFPs can be used in
 CC bioluminescence-generating systems, assays, screening methods, diagnostic
 CC method and articles of manufacture. They can be expressed using
 CC e.g. bacterial, yeast, fungal, plant, insect or animal cells. The Renilla
 CC mulleri, Gaussia and Pleuromamma luciferase or Renilla or Ptiliosarcus
 CC GFPs can be used in e.g. toys, cosmetics, fountain, personal care items,
 CC fairy dust, beverages, soft drinks, foods, textile products, bubbles,
 CC balloons, personal items, dentifrices, soaps, body paints, bubble bath,
 CC ink or paper products. In particular, they can be used in e.g. squirt
 CC guns, pellet guns, finger paints, foot bags, greeting cards, slimy play
 CC material, clothing, bubble making toys, bath powders, cosmetics, body
 CC lotions, gels, body powders, body creams, toiletries, mouthwashes,
 CC soaps, body paints, bubble bath, inks, wrapping paper, gelatins, icings,
 CC frostings, greeting cards, beer, wine, champagne, soft drinks, ice cubes,
 CC ice, dry ice or fountains. The nucleic acids can also be used to produce
 CC transgenic fish and plants.

XX Sequence 1279 BP: 449 A: 234 C: 263 G: 333 T: 0 other:

Query Match 68.9%; Score 760.2; DB 20; Length 1279;

Best Local Similarity 80.5%; Pred. No. 2.2e-175; Matches 1026; Conservative 0; Mismatches 33; Indels 216; Gaps 3;

OY 28 GACAAATGACCGCACGATTTAAAGAACACTGACCTGAAGAGATTTATGCGCAAA 87
 DB 1 GACAAATGACCGCACGATTTAAAGAACACTGACCTGAAGAGATTTATGCGCAAA 60
 OY 88 GCTAGCGTTGAAGAAATGCTGAACATTCACGTTTTTCCATGAGAGATTTGGAAGGC 147
 DB 61 GCTAGCGTTGAAGAAATGCTGAACATTCACGTTTTTCCATGAGAGATTTGGAAGGC 120
 OY 148 AATGATTTATTTGGAAGCAATGATGCAAAATCGGGTTACAAGAGAGAGCTCGCTGCCA 207
 DB 121 AATGATTTATTTGGAAGCAATGATGCAAAATCGGGTTACAAGAGAGAGCTCGCTGCCA 180
 OY 208 TTGCGCTTTGATATTTGTTCCATAGCTTTCCATACGCGAATGCAATGCAAGAAATAC 267
 DB 181 TTGCGCTTTGATATTTGTTCCATAGCTTTCCATACGCGAATGCAATGCAAGAAATAC 240
 OY 268 CCAGAGACATTTGCGGACACTGTTGTTCAATCATCTTCCCGCTGATTTTTCTACGAAGA 327
 DB 241 CCAGAGACATTTGCGGACACTGTTGTTCAATCATCTTCCCGCTGATTTTTCTACGAAGA 300
 OY 328 AATCTACGCTTTGAAGATGCGCCATTTGTTGACATTCGTTGACATATTAAGTTAGAAGAT 387
 DB 301 AATCTACGCTTTGAAGATGCGCCATTTGTTGACATTCGTTGACATATTAAGTTAGAAGAT 360
 OY 388 GATAGTTTCCACTACAAAGTGAATAGAGGCAACGTTTCCCTAGTAACGACCCGTTG 447
 DB 361 GATAGTTTCCACTACAAAGTGAATAGAGGCAACGTTTCCCTAGTAACGACCCGTTG 420
 OY 448 ATGCAAAAAGCCATCTCTGGCATGAGCCATGTTGAGCTGCTTACATGAACAGCCGC 507
 DB 421 ATGCAAAAAGCCATCTCTGGCATGAGCCATGTTGAGCTGCTTACATGAACAGCCGC 480
 OY 508 GTTCTGCTGGCGAAGTACATCTCGTTTCAAACTGACGACGAGACATTAATACGCTG 567
 DB 481 GTTCTGCTGGCGAAGTACATCTCGTTTCAAACTGACGAGACATTAATACGCTG 540
 OY 568 CACATGAAAAGCTTTTACAGATCCAAAGGTGAGTGAAGAAATTTCCGGAATATCACTTT 627
 DB 541 CACATGAAAAGCTTTTACAGATCCAAAGGTGAGTGAAGAAATTTCCGGAATATCACTTT 600
 OY 628 ATCCATCATCTGCTGAGAGAAACCTAGCTGGAAGAAAGCTTCTGGAACACGCGAG 687
 DB 601 ATCCATCATCTGCTGAGAGAAACCTAGCTGGAAGAAAGCTTCTGGAACACGCGAG 660
 OY 688 ACCGCCATTGCAACAAGTACCAATTTGAAAAACCTCTGGGCTCCCTTATGATGATGGTG 747
 DB 661 ACCGCCATTGCAACAAGTACCAATTTGAAAAACCTCTGGGCTCCCTTATGATGATGGTG 720
 OY 748 TAGAAAATGACCAATATATCTGGGAAA----- 774

DB 721 TAGAAAATGACCAATATATCTGGGAAAATCACCATATATCTGGGAAAATGACCAATTTA 780
 OY 775 ----- 774
 DB 781 CTGGGAAAATGACCAATATATCTGTAGAAAATCACCATATATCTGGGAAAATGACCAAT 840
 OY 775 ----- 774
 DB 841 TTATCTGGGAAAATGACCAATTTACTGTAGAAAATCACCATATATCTGTGAAAATGACCA 900
 OY 775 -----CCGATTAACCGTTTGGAGCTT 795
 DB 901 AATATCTGTAGAAATGTTACACACTGGGTGATTAACCGTTTCGATTAACCGTTTGGAGCTT 960
 OY 796 GTGTATACAAATTTATTTGGGCTATTTTGTATATGTGTATGTGTATGATCAATAGA 855
 DB 961 GTGTATACAAATTTATTTGGGCTATTTTGTAAATGTATGTGTGTATGATCTATAGA 1020
 OY 856 CGTGTATTCATCATTGCTTGAATCTTCAGCAAAAGAACCTCGACGATATTGAACCTG 915
 DB 1021 CGTGTATTCATCATTGCTTGAATCTTCAGCAAAAGAACCTCGACGATATTGAACCTG 1062
 OY 916 GAAGCATATTTGAACCTCGACGAGAGCGTAAAGAGACCGCACAAATTAAGCGTTTCAA 975
 DB 1063 GAAGCATATTTGAACCTCGACGAGAGCGATAAAGAGACCGCACGATTAATTAATA 1122
 OY 976 CCAGCATGTTGGAATCTTTTAAACCGATCAAAACGATTAATTAATATATATATACCTGTA- 1034
 DB 1123 CCAGCATGTTGGAATCTTTTAAACCGATCAAAACGATTAATTAATATATATATACCTGTA 1182
 OY 1035 -----TACCTTATATATATCTATATAGTTTGAATGATTAATCTGTTCTGATCAAAA 1089
 DB 1183 CATATATATATATATATATCTTACATAGTTTGAATGATTAATCTGTTCTGATCACTA 1242
 OY 1090 AAAAAAAAAAAAAA 1104
 DB 1243 AAAAAAAAAAAAAA 1257
 RESULT 5
 AAF89810
 ID AAF89810 standard; DNA: 1279 BP.
 XX
 AC AAF89810;
 DT 23-JUL-2001 (first entry)
 DE
 XX
 KW Nucleotide sequence of a green fluorescent protein.
 DE
 XX
 OS Ptiliosarcus gurneyi.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 7..723
 FT /tag= a
 FT /product= "green fluorescent protein (GFP)"
 FT
 PN WO200134824-A2.
 PD 17-MAY-2001.
 PD
 PF 10-NOV-2000; 2000WO-US30915.
 PF
 XX 10-NOV-1999; 99US-0164592.
 XX
 PR (RIGF-) RIGEL PHARM INC.
 PA
 XX
 PI Anderson D;
 PI
 XX
 DR WPI: 2001-329091/34.
 DR P-PSDB: AAB83917.

XX Novel retroviral vector, containing gene encoding Renilla green
PT fluorescent protein, useful as reporter for cell assays, particularly
PT intracellular assays -

XX Example: Fig 3B; 83bp; English.

PS The specification describes a retroviral vector comprising a Renilla
XX green fluorescent protein (pGFP or rGFP) gene. pGFP and rGFP proteins
CC are useful as reporters for cell assays, particularly intracellular
CC assays including methods of screening libraries using pGFP or rGFP, and
CC for screening protein-protein, nucleic acid-protein or nucleic
CC acid-nucleic acid interactions. pGFP or rGFP proteins are also useful
CC in cellular assays, including assays for alterations in exocytosis,
CC cell cycle regulation, apoptosis, cellular proliferation and/or
CC differentiation. pGFP or rGFP proteins are also useful for elucidating
CC bioactive agents that can cause a population of cells either to move
CC out of one growth phase into another, or to arrest in a growth phase.
CC pGFP or rGFP proteins are also useful for screening bioactive agents for
CC their ability to modulate cell cycle regulation, including the activation
CC or suppression of cell cycle checkpoint pathways and ameliorating
CC checkpoint defects. The present sequence encodes pGFP.

XX Sequence 1279 BP; 449 A; 234 C; 263 G; 333 T; 0 other;

SO Query Match 68.9%; Score 760.2; DB 22; Length 1279;

Best Local Similarity 80.5%; Pred.No.2.2e-175;

Matches 1026; Conservative 0; Mismatches 33; Indels 216; Gaps 3;

OY 28 GACAAATGACCGCAGCTATTAAAGAACTGAGTGAAGAGTTATGTCGCAAA 87
Db 1 GACAAATGACCGCAGCTATTAAAGAACTGAGTGAAGAGTTATGTCGCAAA 60
OY 88 GGTACGTTGAAGGATGCTGAACATCAGTTTTCATGGAAGAGTTGGAAAAAGC 147
Db 61 GGTACGTTGAAGGATGCTGAACATCAGTTTTCATGGAAGAGTTGGAAAAAGC 120
OY 148 AATGATATTATTGGAACCAATTTGATGCAAAATCCGGGTTTCAAAAGGAGGCGTTGCCA 207
Db 121 AATGATATTATTGGAACCAATTTGATGCAAAATCCGGGTTTCAAAAGGAGGCGTTGCCA 180
OY 208 TTGCGCTTGGATATTGTTTCCATAGCTTTCGCAATACGGGAATGCACTTTCACGAAATAC 267
Db 181 TTGCGCTTGGATATTGTTTCCATAGCTTTCGCAATACGGGAATGCACTTTCACGAAATAC 240
OY 268 CCAGACGACATTCGCGACTACTTGTTCATCATTCGCCGCTGGATTTTTCACGAAAGA 327
Db 241 CCAGACGACATTCGCGACTACTTGTTCATCATTCGCCGCTGGATTTTTCACGAAAGA 300
OY 328 AATCTACGCTTTGAAGATGGCGCATTTGTCATTCGTTCAAGATATAAGTTAGAGAT 387
Db 301 AATCTACGCTTTGAAGATGGCGCATTTGTCATTCGTTCAAGATATAAGTTAGAGAT 360
OY 388 GATAAGTTCCTACATAAGATGAGTATAGAGCAGCGTTTCCCTAGTACGAGCCCGTG 447
Db 361 GATAAGTTCCTACATAAGATGAGTATAGAGCAGCGTTTCCCTAGTACGAGCCCGTG 420
OY 448 ATGCAAAAAAGCCATCTCGCGATGAGCGCATGCTTGGAGTGGTCTACATGACAGCGCG 507
Db 421 ATGCAAAAAAGCCATCTCGCGATGAGCGCATGCTTGGAGTGGTCTACATGACAGCGCG 480
OY 508 GTTCTGGTGGGGAAGTAGATCTGTTTCAAACTGCACTGAGGGAATATTACTGCTGC 567
Db 481 GTTCTGGTGGGGAAGTAGATCTGTTTCAAACTGCACTGAGGGAATATTACTGCTGC 540
OY 568 CACATGAAAAAGCTTTTACAGATCCAAAGGTGAGTGAAGAAATTCGCGAATATCACTTT 627
Db 541 CACATGAAAAAGCTTTTACAGATCCAAAGGTGAGTGAAGAAATTCGCGAATATCACTTT 600
OY 628 ATCCATCATCGTCTGGAGAAACCTACGTGAAGAAAGAACTGCTGGAACACACGAG 687
Db 601 ATCCATCATCGTCTGGAGAAACCTACGTGAAGAAAGAACTGCTGGAACACACGAG 660

OY 688 ACGGCCATTTCACCAACCTGACCAATTTGGAAAAACCTCTGGGCTCCCTTCATGATGGTG 747
Db 661 ACGGCCATTTCACCAACCTGACCAATTTGGAAAAACCTCTGGGCTCCCTTCATGATGGTG 720
OY 748 TAGAAAAATGACCAATATACTGGGGA----- 774
Db 721 TAGAAAAATGACCAATATACTGGGGAATAATCACCATATACTGGGGAATAATGACCAATTTA 780
OY 775 ----- 774
Db 781 CTGGGGAATAATCACCATATACTGTAAGAAATCACCATATACTGGGGAATAATGACCAAT 840
OY 775 ----- 774
Db 841 TTACTGGGGAATAATGACCAATTTACTGTAGAAATATCACCATATACTGGGGAATAATGACCA 900
OY 775 -----CCGATAACCGTTTGAAGCTT 795
Db 901 AATACTGTAGAAATGTTCCACACTGGGTTGATTAACCGTTTGCATTAACCGTTTGAAGCTT 960
OY 796 GGTATATACAAATTTATTTGGGCTCATTTTGTATGTATGTATGTATGTATGTATGTATGTAT 855
Db 961 GTGTATACAGTTATTTGGGCTCATTTTGTATGTATGTATGTATGTATGTATGTATGTATGA 1020
OY 856 CGTCGTATTCATAGCTTGAATCCTTCACAGCAAAAGAACCTCGAAGCATTTGAACCTC 915
Db 1021 CGTCGTATTCATAGCTTGAATCCTTCACAGCAAAAGAACCTCGAAGCATTTGAACCTC 1062
OY 916 GAAGCATATTGAAACCTGACGAGAGCGTAAAGAGACCGCAAAATTTACCGCTTTCA 975
Db 1063 GAAGCATATTGAAACCTGACGAGAGCGATAAAGAGACCGCAAAATTTAATA 1122
OY 976 CCAGCAGTTGGAATCTTTAAACGATCAAAACATTTAATATATATATATATATATATATATAT 1034
Db 1123 CCAGCAGTTGGAATCTTTAAACGATCAAAACATTTAATATATATATATATATATATATATAT 1182
OY 1035 -----TACTTATATATATCTATATATAGTTTGAATTTGAATTTGAATTTGAATTTGAATTTGA 1089
Db 1183 CATATATATATATATATATCTACATAGTTTGAATTTGAATTTGAATTTGAATTTGAATTTGA 1242
OY 1090 AAAAAAAAAAAAAA 1104
Db 1243 AAAAAAAAAAAAAA 1257

RESULT 6
AAD22208
ID AAD22208 standard: DNA; 1279 BP.
XX
XX AAD22208;
AC
XX
DT 12-FEB-2002 (first entry)
XX
DE Ptiliosarcus gurneyi green fluorescent protein encoding DNA #2.
XX
XX Green fluorescent protein: GFP; bioluminescence generating system; toy;
KW luciferase; finger paint; slimy play material; fishing lure; sparkler;
KW doll; balloon; personal care item; cosmetic; bath powder; body cream;
KW tooth paste; mouth wash; soap; body paint; ornamental transgenic plant;
KW bubble bath; fountain; fairy dust; food; gelatin; icing; frosting; beer;
KW wine; champagne; milk; soft drink; ice cube; ice; foot bag; beverage;
KW dry ice; textile; clothing; paper product; greeting card; wrapping paper;
KW ds.
XX
OS Ptiliosarcus gurneyi.
XX
XX
XX Key Location/Qualifiers
FH 7.723
FT CDS /tag= a
FT /product= "P. gurneyi green fluorescent protein"
XX
XX WO200168824-A2.
XX

XX W09949019-A2.
 PN 30-SEP-1999.
 PD 26-MAR-1999; 99WO-US06698.
 XX 27-MAR-1998; 98US-0079624.
 PR 15-JUN-1998; 98US-0089367.
 PR 01-OCT-1998; 98US-0102939.
 XX (PROL-) PROLUME LTD.
 PA (BRYA/) BRYAN B J.
 XX Bryan BJ, Szent-Gyorgyi C;
 PI WPI: 1999-580443/49.
 DR P-PSDB: AAY39950.
 XX New isolated Renilla mulleri, Gaussia and Pleuromamma luciferase and
 PT Renilla and Ptilosarcus green fluorescent protein nucleic acids -
 XX Claim 36; Page 215-216; 233pp; English.

This sequence encodes a green fluorescent protein of the invention. The invention relates to Renilla mulleri, Gaussia and Pleuromamma luciferase and Renilla and Ptilosarcus green fluorescent protein (GFP) nucleic acids and proteins. The luciferases and GFPs can be used in bioluminescence-generating systems, assays, screening methods, diagnostic method and articles of manufacture. They can be expressed using e.g. bacterial, yeast, fungal, plant, insect or animal cells. The Renilla mulleri, Gaussia and Pleuromamma luciferase or Renilla or Ptilosarcus GFPs can be used in e.g. toys, cosmetics, fountains, personal care items, fairy dust, beverages, soft drinks, foods, textile products, bubbles, balloons, personal items, dentifrices, soaps, body paints, bubble bath, ink or paper products. In particular, they can be used in e.g. squirt guns, pellet guns, finger paints, foot bags, greeting cards, slimy play material, clothing, bubble making toys, bath powders, cosmetics, body lotions, gels, body powders, body creams, toothpastes, mouthwashes, soaps, body paints, bubble bath, inks, wrapping paper, gelatins, icings, frostings, greeting cards, beer, wine, champagne, soft drinks, ice cubes, ice, dry ice or fountains. The nucleic acids can also be used to produce transgenic fish and plants.

Sequence 1079 BP: 375 A; 176 C; 209 G; 319 T; 0 other:

Query Match 35.7%; Score 394.2; DB 20; Length 1079;
 Best Local Similarity 71.4%; Pred. No. 2.8e-86;
 Matches 519; Conservative 0; Mismatches 208; Indels 0; Gaps 0;

QY 27 AGACAAATGAGACCGGACGCTATTAAAGAACACTGAGCTGAAGAGATTATGCGGCANA 86
 DB 252 AGATAAGATGAGTAAAGCAATATTGAGAACACTGTTTACAGAGATATGCGATATA 311
 QY 87 AGCTAGCGTTGAAGAAATCGTAACAATCGTTTTTTCATGGAAGATTTGGAAAGG 146
 DB 312 AGTAATATCGGAAGAAATGTAACACACATGTTTTTACAATGAGAGGTTGGGGCAAG 371
 QY 147 CAATGATTATTGGAACCAATTGATGCAATCCGGGTACAAAGGAGTCGTTGCC 206
 DB 372 GAATATTTTATTCGCAATCACTGGTTCAGATTCTGTCACAGAAAGGGGCCCACTGCC 431
 QY 207 ATTGCGTTTCGATATGTTTCATACCTTCATAGCGGAATGCGCATTTACGCAATA 266
 DB 432 TTTTGATTGATTTGTTGTCACACCTTTTCAATATGCAACCGCTTTCACGAAATA 491
 QY 267 CCCAGACGATTTGGCGACTACTTTGTTCAATCATTCGCCGTGATTTTTCACGAAG 326
 DB 492 TCCGAATGATATATCAGATTATTTTATACATCATTTTCCACGACGATTTATGATACG 551
 QY 327 AATTCAGCGTTTGAAGATGCGCCATTTGTGACATTCGTTAGATATAGTTTACAGA 386
 DB 552 AACATTACCTTACGAAGATGCGGACTGTGAAATTCGTTCAATATTAATTAATTAAGA 611

QY 387 TGATAGTTCCACTCAAAAGTGAGATATAGAGCAACGGTTTCCCTAGTAACGACCGT 446
 DB 612 AGACAGTTTCGTCTACAGATGGAATACAAAGGTACTTAACCTTCCAGATGTCCTCGT 671
 QY 447 GATGCAAAAAGCCATCTTCGCGATGAGCCATCGTTTGAGTGTCTACATGAGACGCG 506
 DB 672 CATGCAAGAACTATCTTATGGAATAGAGCTTCATTTAGAGCCATGTACATGAATATGG 731
 QY 507 CGTTTGGTGGCGGAAGTATGATCTGTTTACAAACTCCAGTACAGGAATATTACTCGT 566
 DB 732 CGTTTGGTGGCGGAAGTATGATCTCTCTATTAACATAACTCTGGGAAATATTATTCATG 791
 QY 567 CCACATGAAGACGTTTACAGATCCAAAGCTGAGTGAAGAAGATTCCCGCAATATACACT 626
 DB 792 TCACATGAAGAAACATTATATAGTACGAAGGTAGTAAAGAGTTCTCTCGTATCATTT 851
 QY 627 TATCCATCATCTCTGAGAAACCTACCTGAGAGAGAACCTTCGTGGAACAACACGA 686
 DB 852 TATTCACATCTGTTTGAAAGACCTTACCTAGACAGCGGGGTTGCTTGAACAGATGA 911
 QY 687 GACGGCCATTGCAACACTGACCAACATTTGGAACCTCTGGCTCCCTTCATGAATGCT 746
 DB 912 GACTGCTATTCCTCAAAATGACATCTATACGAAGAACCACTAGACTCCTTACACGAATGGT 971
 QY 747 GTAGAAA 753
 DB 972 TTAAACA 978

RESULT 8
 AAF89808
 ID AAF89808 standard: DNA; 1079 BP.

AAF89808:

23-JUL-2001 (first entry)

Nucleotide sequence of Renilla green fluorescent protein.

XX Retroviral vector: Renilla; green fluorescent protein; pGFP; rGFP; ss.

XX Key Location/Qualifiers
 FH 259..975 /*tag= a
 FT CDS /product= "green fluorescent protein (rGFP)"
 FT

OS Renilla mulleri.

PN W0200134824-A2.

PD 17-MAY-2001.

PF 10-NOV-2000; 2000WO-US30915.

PR 10-NOV-1999; 99US-0164592.

PA (RIGE-) RIGEL PHARM INC.

PI Anderson D;

DR WPI: 2001-329091/34.

PT P-PSDB: AAB83915.

XX Novel retroviral vector, containing gene encoding Renilla green

PT fluorescent protein, useful as reporter for cell assays, particularly

PS intracellular assays -

XX Example; Fig 2; 83pp; English.

XX The specification describes a retroviral vector comprising a Renilla

CC green fluorescent protein (pGFP or rGFP) gene. pGFP and rGFP proteins

are useful as reporters for cell assays, particularly intracellular

assays including methods of screening libraries using pGFP or rGFP, and
 CC for screening protein-protein, nucleic acid-protein or nucleic
 CC acid-nucleic acid interactions. pGFP or rGFP proteins are also useful
 CC in cellular assays, including assays for alterations in exocytosis,
 CC cell cycle regulation, apoptosis, cellular proliferation and/or
 CC differentiation. pGFP or rGFP proteins are also useful for elucidating
 CC bioactive agents that cause a population of cells either to move
 CC out of one growth phase into another, or to arrest in a growth phase.
 CC pGFP or rGFP proteins are also useful for screening bioactive agents for
 CC their ability to modulate cell cycle regulation, including the activation
 CC or suppression of cell cycle checkpoint pathways and ameliorating
 CC checkpoint defects. The present sequence encodes rGFP.

Sequence 1079 BP; 375 A; 176 C; 209 G; 319 T; 0 other;

Query Match 35.7%; Score 394.2; DB 22; Length 1079;
 Best Local Similarity 71.4%; Pred. No. 2.8e-86;
 Matches 519; Conservative 0; Mismatches 208; Indels 0; Gaps 0;

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OY 27 AGACAAATGACCCGACGTATTAAAGAACACTGACCTGAAGAGATTATGTCGGCAA 86
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 252 AGATGAATGATGATTAACAAATATTGAAGAACACTGTTTCAAGAACTATGTCGTATA 311
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 87 AGCTACGTTGAAGAAATCGTGAACAATCAGTTTTTCCATGGAAGATTGGAAAAG 146
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 312 AGTAAATCTGGAAGAAATGTAACAACCATGTTTACAAATGAGAGGTTGCGGCAAG 371
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 147 CATTGATTATTGGAACCAATTGATGCAATCCGGGTTACAAAGAGCGTCGTTGCC 206
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 372 GAATATTATTATGCGCAATCACTGGTTCAGATTGCTGTCAGCAAAAGGCGCCACAT 431
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 207 ATTCCGTTTCGATATTGTTTCCATACCTTCATACCGGATTCGATTCGCAATA 266
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 432 TTTTGCAATTGATATTGTGTACACAGCTTTTCAATATGCAACCTGACTTTCAGAAATA 491
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 267 CCCAGACCAATTCGGACTACTTTCATGATTCGCCGGTGGATTTTTCAGCAAG 326
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 492 TCCGATGATATATCAGATTATTTTACATCATTTCCAGAGATTATGATGACG 551
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 327 AATTCACGCTTGAAGATTCGCCCATTTGTCGATTCCTTCAGATATAAGTTTACAG 386
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 552 AACATTACCTTACGAAGATGCGCGCTGTGTAATTCCTTCAGATATAATTAATAGA 511
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 387 TGATAGTTCCACTCAAGATGAGTATAGAGCAACGGTTTCCCTAGTAACGGACCG 446
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 612 AGACAGATTCGCTTACAGACTGSAATACAAAGTAGTAAGTTCCAGATGATGTCCT 671
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 447 GATGCAAAAAGCCATCTCGGCATGAGCCCATGTTGAGTGCTTACATGAACACG 506
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 672 CATGCAAGACTATCTTAGAATAGAGCTTCATTTGAAGCCATGACATGAATATG 731
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 507 CGTTTCGGGGGGAGTAGTATGCTTTTACAAACTCGAGTCAGGAGACATTAATCTG 566
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 732 CGTTTCGGGGGGAGTAGTATGCTTTTACAAACTCGAGTCAGGAGACATTAATCTG 791
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 567 CCACATGAACACGCTTTACAGATCCAAGGTGAGTGAAAGTAATCCCGAATATCAT 826
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 792 TCACATGAACAAACCTTAATGAAGTCGAAGGTCTAGTAAGAGACTTTCTTCGATCAT 851
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 627 TATCATCATCGCTTGAGAAACCTTACGTGGAAGAAGAGAGTCTGTCGACACAGCA 866
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 852 TATTCACATCGTTTGGAAAGACCTTACAGACGCGCGCTGCTGTGAACAGCATGA 911
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 687 GAGCGCATTTGACACACTGACCACTTGGAAAGCTCTGGCTTCCTTCATGATAGGCT 746
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 912 GACTGCTATTTCCTCAATGACATCTATAGGAAACCACTAGAGATCCTTACACGAATCG 971
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 747 GTAGAAA 753
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 972 TTTAAACA 978
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 9

AAD22198
 ID AAD22198 standard; DNA; 1079 BP.
 XX
 AC AAD22198:
 XX
 DT 12-FEB-2002 (first entry)
 XX
 DE Renilla mulleri green fluorescent protein encoding DNA.
 XX
 KW Green fluorescent protein; GFP; bioluminescence generating system; toy;
 KW luciferase; finger paint; slimy play material; fishing lure; sparkler;
 KW doll; balloon; personal care item; cosmetic; bath powder; body cream;
 KW looth paste; mouth wash; soap; body paint; ornamental transgenic plant;
 KW bubble bath; fountain; fairy dust; food; gelatin; icing; frosting; beer;
 KW wine; champagne; milk; soft drink; ice cube; ice; foot bag; beverage;
 KW dry ice; textile; clothing; paper product; greeting card; wrapping paper;
 KW ds.
 OS Renilla mulleri.
 XX
 FH Key Location/Qualifiers
 FT CDS 259..975
 FT /*tag= a
 FT /product= "Renilla mulleri green fluorescent protein"
 PN MO200168824-A2.
 XX
 PD 20-SEP-2001.
 PF
 PF 15-MAR-2001; 2001MO-US08277.
 PF
 PR 15-MAR-2000; 2000US-189691P.
 XX
 PA (PROL-) PROLUME LTD.
 PA (BRYA/) BRYAN B J.
 XX
 PI Bryan BJ, Szent-Gyorgyi C, Szczepaniak W:
 DR WPI; 2002-010561/01.
 DR P-PSDB; ABE13380.
 XX
 PT Nucleic acids encoding Renilla reniformis green fluorescent proteins,
 PT useful in diagnostic bioluminescence procedures -
 XX
 PS Disclosure; Page 156-157; 175pp; English.
 XX
 CC The patent discloses sea pansy (Renilla reniformis) green fluorescent
 CC proteins (GFP) and their corresponding polynucleotides. The invention
 CC also relates to sequences of the bioluminescence generating system
 CC (e.g. luciferase). R. reniformis GFP are used in diagnostic methods
 CC and in the production of novelty items such as toys (e.g. squirt gun,
 CC pellet gun, toy "Halloween" eggs, toy cigarettes, board/card game
 CC toys), finger paints, slimy play material, bubbles in bubble making
 CC toys, fishing lures, dolls, sparklers, magic wand toys, balloons,
 CC personal care item (e.g. cosmetic, bath powders, body creams, tooth
 CC pastes, mouth wash, soaps, body paints, bubble bath), ornamental
 CC transgenic plants, fountain, fairy dust, food (gelatins, icings,
 CC frosting, beers, wine, champagne, milk, soft drinks, ice cubes, ice,
 CC dry ice, beverage), textile (foot bag, clothing) and/or paper product
 CC (greeting cards, wrapping paper). The present sequence is a DNA
 CC encoding Renilla mulleri green fluorescent protein.

Sequence 1079 BP; 375 A; 176 C; 209 G; 319 T; 0 other;

Query Match 35.7%; Score 394.2; DB 24; Length 1079;
 Best Local Similarity 71.4%; Pred. No. 2.8e-86;
 Matches 519; Conservative 0; Mismatches 208; Indels 0; Gaps 0;

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OY 27 AGACAAATGACCCGACGTATTAAAGAACACTGACCTGAAGAGATTATGTCGGCAA 86
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 252 AGATGAATGATGATTAACAAATATTGAAGAACACTGTTTCAAGAACTATGTCGTATA 311
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 87 AGCTACGTTGAAGAAATCGTGAACAATCAGTTTTTCCATGGAAGAGATTGGAAAAG 146
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 312 AGTAATCTGAGAGAAATGTAAACACCAATCTTTTACAAATGAGGCGTGGCGCAAGG 371
Oy 147 CAATCTATTATTATTTGGAACCAATTCATCGCAATTCGGGGTTACAAAGGAGTCCGTTGCC 206
Db 372 GAAATATTTATTCGCGCAATCAACTGTTGAGATTCGTGCAGAAAGGGGGCCCACTGCC 431
Oy 207 ATTCCTTCGATTTGTTTCATAGCTTTTCCATACGAGGAATCCGACTTTTCACAAATA 266
Db 432 TTTTCATTTGATTTGTTGTCACGAGCTTTTTCATATGGAACCCGACTTTTCAGAAATA 491
Oy 267 CCCAGAGCAATTTGGGACCTACCTTTGTTCAATCATTTCCCGCTGGATTTTCTACGAAG 326
Db 492 TCCGAAATGATATATGATATTTATTAACAATCATTTCCAGAGAGATTATGATATGAACG 551
Oy 327 AAATCTAGCCTTGAAGATGGCGCATTCCTTGACATTCCTTGAGTATTAAGTTAGAAANA 386
Db 552 AACATTACGCTTACGAAGATGGGAGCTTGTGAAATTCGCTTCAGATATTAATTTATAGA 611
Oy 387 TGATTAAGTTCCACTACAAAGTGAGTATAGAGCAACGGTTCCCTAGTAACGACCCGT 446
Db 612 AGACAAAGTTTCGCTACAGAGTGAATACAAAGTAGTAACTTCCAGATGATGTCGCT 671
Oy 447 GATGCAAAAAGCCATTCCTGCGCATGAGCCATCGTTGAGTGTGCTACATGAAACAGCGG 506
Db 672 CATGCAAGAACTATCTTAGAATAGAGCTTCATTTGAAAGCCATGATCATGAATATAG 731
Oy 507 CGTCTGGGGGGAAGTATGATCTGTTTACAAACCTCGATGAGGGAATATATCTACGCTG 566
Db 732 CGTCTGGTGGCGGAATATCTGTCTATTAACCTAGCTGGGAATATATTTATCATG 791
Oy 567 CCACATGAAACGTTTACAGATCCAAAGTGAGTGAAGAATTCGCCGAATATCACTT 626
Db 792 TCACATGAAACATTAATGAAGTGAAGGTGATGAAGAGTTTCCCTGATCATATT 851
Oy 627 TATTCATCATCTCTGAGCAAAAACCTAGCTGGAAGAGAACCTTCGTGAACACACACA 686
Db 852 TATTCACATCTCTTGGAAAAGACTTACCTAGACAGCGGGGGTTCGTTGAACAGCATGA 911
Oy 687 GAGGCGCATTTGACAACTGACCAATTTGAAAACCTCGGGGCTCCCTCATGAATGGGT 746
Db 912 GACTGCTATTTGCTCAATATACATCTATAGGAAAACCACTAGATCCTTACAGCAATGGGT 971
Oy 747 GTAGAAA 753
Db 972 TTAAACA 978

RESULT 10
ABO73693
ID ABO73693 standard; DNA; 720 BP.
XX ABO73693;
AC
XX
XX
XX 07-OCT-2002 (first entry)
DE Renilla reniformis green fluorescent protein nucleotide SEQ ID NO:1.
XX
XX Renilla reniformis; green fluorescent protein; GFP; fluorescence;
KM fusion protein; intramolecular dimer fluorescent protein; IDFP; FACS;
KM multimeric protein; fluorescence activated cell sorting; cell population;
KM viral vector infection; fluorescence resonance energy transfer; FRET;
KM transgene expression; protein:protein interaction; gene; ds.
XX
XX Renilla reniformis.
OS
XX
XX Key Location/Qualifiers
FH 1..720
FT CDS
FT /tag= a
FT /product= "green fluorescent protein"
FT /transl_except= (pos:1..6,aa:Met)
FT /transl_except= (pos:358..360,aa:Gln)
XX

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PN W0200248174-A2.
XX
XX 20-JUN-2002.
XX
XX 13-DEC-2001; 2001WO-US48690.
XX
XX 15-DEC-2000; 2000US-256121P.
XX
XX (STRA-) STRATAGENE.
PI
PI Davila RM, Vaillancourt P;
XX
XX WPI: 2002-583482/62.
DR P-PSDB; ABP51820.
XX
XX
XX Novel recombinant fusion polypeptide which is fluorescent when excited,
XX comprising first polypeptide peptide-bonded to second polypeptide, the
XX polypeptides being found in nature as monomers of a multimeric protein
XX
XX
XX Disclosure; Fig 1; 59pp; English.
XX
XX The present invention describes a recombinant fusion polypeptide
XX (intramolecular dimer fluorescent protein (IDFP)) (1) comprising a first
XX polypeptide peptide-bonded to a second polypeptide, where the first and
XX second polypeptides are found in nature as monomers of a multimeric
XX protein and the first and second polypeptides are not fluorescent donor
XX and acceptor to each other, and (1) is fluorescent when excited. (1) is
XX useful for monitoring the interaction of two polypeptides of interest
XX which involves contacting a first polypeptide and the second polypeptide.
XX (1) is also useful for screening for a compound that modulates the
XX interaction of first and second member of specific binding pair which
XX involves contacting a first polypeptide and a second polypeptide in the
XX presence and absence of candidate modulator. (1) can be used as reporter
XX genes to monitor the activity of promoter sequences to investigate the
XX cellular localisation of fusion proteins; to mark cellular proteins for
XX fluorescence activated cell sorting (FACS) analyses of cell population,
XX to monitor viral vector infection, to monitor transgene expression
XX in vivo or in culture, and to monitor protein:protein interactions both
XX in vivo and in vitro. (1) is suitable for applications that rely on
XX fluorescence resonance energy transfer (FRET). The present sequence
XX encodes Renilla reniformis green fluorescent protein (GFP), which is
XX given in the exemplification of the present invention.
XX
XX Sequence 720 BP; 223 A; 122 C; 169 G; 206 T; 0 other;
XX
XX Query Match 35.6%; Score 392.6; DB 24; Length 720;
XX Best Local Similarity 72.4%; Pred. No. 6,2e+86;
XX Matches 509; Conservative 0; Mismatches 194; Indels 0; Gaps 0;
Oy 47 TATTAAGAACACTGAGCTGAAGAATTTATGTGGCAAAAGCTAGCGTTGAAGGAATCG 106
Db 17 TATTAAGAACACTGAGCTGAAGAATTCATGCTTTAAAGTAATCGAAGGTGAG 76
Oy 107 TGAACATACGCTTTTTCATGGAAGCATTTTGAAAGGCAATGATATTATTTGGAAC 166
Db 77 TAAACATATCATGTGTCAACATGAAGGTTGTGAAAAGAAATATTTATTCGGAAC 136
Oy 167 AATTGATGCAAAATCCGGGCTTACAAAGGAGGAGTCCGTTGCTTGGCTTTCGATATTGTT 226
Db 137 AACTGTTAGATCTGTGCACAAAGGGGCTCCGCTTCATTTGATTTGATTTCTCT 196
Oy 227 CCATAGCTTTCGAATACGGAATCCGACTTTGACGAATATCCAGAGCATTTGGCGACT 286
Db 197 CACGACCTTTCGAATACGGAATCCGACTTTCAGGAATATCCGAGAGTATATGAGACT 256
Oy 287 ACTTTGTTCAATCATTCCCGCTGATTTTTCAGGAAGAAATCTAGCCTTTGAAGATG 346
Db 257 TTTTATCAAAATCATTTCCAGCGGATTTGTATACGAAGAAAGCTTGCCTTACGAAGATG 316
Oy 347 GCGGCATTTGTCACATCTGCTTCAGATATAGTTTACAATATATTAAGTCCACTACAAG 406
Db 317 GTGGAAGTGTGAAGTCCGTGAGATATTAATTTATTCAGAGAGATTTGCTACAGAG 376

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Db      617 AGACTGATGTGGAAGAGGAGTTTGTGACGAACGACGCGCATTTGCTCACTGA 676
Oy      707 CCACAAATTGGAACCTCTGGCGCTTCATGATGAATGGGTGA 749
Db      677 CATCGTGGGAAACCACTTGATCTTACACGAAATGGGTTTA 719

RESULT 12
AAS14038
ID      AAS14038 standard; cDNA: 720 BP.
XX
AC      AAS14038;
XX
DT      18-Dec-2001 (first entry)
XX
DE      R. reniformis humanised cDNA encoding Green fluorescent protein, GFP.
KM      Green fluorescent protein; GFP; ss: gene therapy; FACS analysis; mutant;
KW      protein-protein interaction; Fluorescence activated cell sorting.
XX
OS      Renilla reniformis.
OS      Synthetic.
XX
FH      Key
FH      CDS
FT      1..720
FT      /tag= a
FT      /product= "GFP"
FT      /transl_except= (pos:391..393,aa:Ser)
FT      /replace (9,T)
FT      /tag= b
FT      /replace (12,A)
FT      /tag= c
FT      /replace (15,A)
FT      /tag= d
FT      /replace (18..19,AT)
FT      /tag= e
FT      /replace (30,T)
FT      /tag= f
FT      /replace (33..34,AT)
FT      /tag= g
FT      /replace (49..51,TCG)
FT      /tag= h
FT      /replace (54,T)
FT      /tag= i
FT      /replace (57,A)
FT      /tag= j
FT      /replace (63,T)
FT      /tag= k
FT      /replace (69,A)
FT      /tag= l
FT      /replace (72,T)
FT      /tag= m
FT      /replace (75,A)
FT      /tag= n
FT      /replace (78,T)
FT      /tag= o
FT      /replace (84,T)
FT      /tag= p
FT      /replace (87,T)
FT      /tag= q
FT      /replace (96,A)
FT      /tag= r
FT      /replace (102,A)
FT      /tag= s
FT      /replace (105,T)
FT      /tag= t
FT      /replace (108,T)
FT      /tag= u
FT      /replace (111,A)
FT      /tag= v
FT      /replace (114,A)
FT      /tag= w
FT      /tag= w
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```
FT      mutation
FT      /tag= x
FT      /replace (117,A)
FT      /tag= y
FT      /replace (120,T)
FT      /tag= z
FT      /replace (123..124,TT)
FT      /tag= aa
FT      /replace (126,A)
FT      /tag= ab
FT      /replace (132,A)
FT      /tag= ac
FT      /replace (138,T)
FT      /tag= ad
FT      /replace (150,T)
FT      /tag= ae
FT      /replace (153,C)
FT      /tag= af
FT      /replace (156,A)
FT      /tag= ag
FT      /replace (159,A)
FT      /tag= ah
FT      /replace (162,G)
FT      /tag= ai
FT      /replace (165,T)
FT      /tag= aj
FT      /replace (168,G)
FT      /tag= ak
FT      /replace (171,T)
FT      /tag= al
FT      /replace (174,G)
FT      /tag= am
FT      /replace (177,T)
FT      /tag= an
FT      /replace (180,T)
FT      /tag= ao
FT      /replace (183,A)
FT      /tag= ap
FT      /replace (186,T)
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FT      /replace (189,T)
FT      /tag= ar
FT      /replace (192,T)
FT      /tag= as
FT      /replace (195..198,CTCA)
FT      /tag= at
FT      /replace (201,A)
FT      /tag= au
FT      /replace (204,T)
FT      /tag= av
FT      /replace (210,A)
FT      /tag= aw
FT      /replace (222,T)
FT      /tag= ax
FT      /replace (225,A)
FT      /tag= ay
FT      /replace (231,G)
FT      /tag= az
FT      /replace (234,A)
FT      /tag= ba
FT      /replace (240,G)
FT      /tag= bb
FT      /replace (249..252,ATCA)
FT      /tag= bc
FT      /replace (258,T)
FT      /tag= bd
FT      /replace (261,T)
FT      /tag= be
FT      /replace (264,A)
FT      /tag= bf
FT      /replace (267..270,ATCA)
FT      /tag= bg
FT      /replace (273,T)
FT      /tag= bh
FT      /replace (276,A)
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FT mutation /*tag= bh
FT replace (279,G)
FT /*tag= b1
FT replace (282,A)
FT /*tag= bj
FT mutation replace (285,T)
FT /*tag= bk
FT mutation replace (288,A)
FT /*tag= b1
FT mutation replace (294..295,AA)
FT /*tag= bm
FT mutation replace (297,A)
FT /*tag= bn
FT mutation replace (300..301,CT)
FT /*tag= bo
FT mutation replace (306,T)
FT /*tag= bp
FT mutation replace (312,A)
FT /*tag= bq
FT mutation replace (315,T)
FT /*tag= br
FT mutation replace (318,T)
FT /*tag= bs
FT mutation replace (321,T)
FT /*tag= bt
FT mutation replace (327,T)
FT /*tag= bu
FT mutation replace (330,A)
FT /*tag= bv
FT mutation replace (336..339,TTCA)
FT /*tag= bw
FT mutation replace (342,T)
FT /*tag= bx
FT mutation replace (345,A)
FT /*tag= by
FT mutation replace (348..349,TT)
FT /*tag= bz
FT mutation replace (351,A)
FT /*tag= ca
FT mutation replace (256,T)
FT /*tag= cb
FT mutation replace (369,C)
FT /*tag= cc
FT mutation replace (373,A)
FT /*tag= cd
FT mutation replace (375,A)
FT /*tag= ce
FT mutation replace (381,A)
FT /*tag= cf
FT mutation replace (384,T)
FT /*tag= cg
FT mutation replace (387,A)
FT /*tag= ch
FT mutation replace (390..391,TA)
FT /*tag= ci
FT mutation replace (393,T)
FT /*tag= cj
FT mutation replace (402,G)
FT /*tag= ck
FT mutation replace (405,T)
FT /*tag= cl
FT mutation replace (408,T)
FT /*tag= cm
FT mutation replace (411,T)

Query Match 30.1% Score 332.6; DB 22; Length 720;
Best Local Similarity 56.6% Pred. No. 2.5e-71;
Matches 476; Conservative 0; Mismatches 239; Indels 0; Gaps 0;

OY 35 TGAACCGACGATATTAAAGACACTGACGTGAAGACATTTCGCGCAAAAGCTAGG 94
DB 5 TGAGCAAGCAGATCTCTGAGAGACCGGCTTCAGAGATCATGAGCTTCAAGTGAACC 64
```

```
OY 95 TTGAAGAAATCGTGAACAATCACGTTTTTTCATGAGAGATTTGGAAAGCAATGAT 154
DB 65 TGSAGGGCGGTGGTGAACAACACAGTGTTCACCATGAGGGCTCCGCAAGGACATCC 124
OY 155 TATTTGAAACCAATTTGATGCAAAATCCGGGTTACAAAGGAGGTCCGTTGCATTG 214
DB 125 TGTTCGCAACACGAGTGTGTGAGATCCGCTGACCAAGGGCGCCCTGCTCCCTGGCCT 184
OY 215 TCGATATTGTTTCCATAGCTTTCCATACGGGAATGCACTTTCACGAATACCCGACG 274
DB 185 TCGACATCTGAGCCCGCTTCACATGACGCAACCGACCTTCCACCAATCCCGAGG 244
OY 275 ACATTGCGACTACTTGTGTTCAATCATTCGCGGCTGATTTTCTCGAAGAATCTAC 334
DB 245 ACATCAGCGACTTCTTCATCCAGAGCTTCCCGCGGCTTCGTGTACGAGCGACCTTCG 304
OY 335 GCTTTGAGATGGCGCCATTGTTGACATTTCGTACATATAAGTTTGAAGATGATAGT 394
DB 305 GCTACGAGAGCGCGGCTGTGTGAGATCCGACGACATCAACTGATCGAGGACATGT 364
OY 395 TCCACTACAAAGTGGAGTATAGAGGCAACGGTTTCCTAGTAAAGGACCCGTGATGCA 454
DB 365 TCGTGTACCGCGGTGAGTCAAGGGCGCACCTTCCCAACGCGGCCCGTGTATGAAGA 424
OY 455 AAGCCATCTCCGCGCATGGAGCCATGCTTGGAGGTGTACATGACAGCGGCTCTGG 514
DB 425 AGACCATCACCGGCTTCGACGCCAGCTTGAGGTGTGTACATGACAGCGGCTGTGG 484
OY 515 TGGCGCAAGTAGATCTGTTTACAAACCTGAGTCAAGGAATATTACTGTCACATGA 574
DB 485 TGGGCCAGGTGATCGTGTTACCGCTGACACCGGCAAGTTTACACTGCGCAATCC 544
OY 575 AAACGTTTACAGATCCAAAGGTGAGTGAAGAATTTCCCGGAATATCATTTATCATC 634
DB 545 GCACCTGTATGAAGACCAAGGGCGTGTGTAAGGACTTCCCGAGTACCACTTCATCCAC 604
OY 635 ATGCTGTGAGAAACCTGCTGGAAGAAGAACTTCTGGAAACAACGAGAGCGCA 694
DB 605 ACCGCTTGAGAAAGACCTACGTGAGAGACGGCGCTTCCTGGAGCAACGAGACCGCA 664
OY 695 TTGCACACTGACACCAATTTGAAAAACCTGTGGGCTCCCTCATGATGGGTGA 749
DB 665 TCGCCAGCTGACACAGCCCTGGCAAGCCCTCGGACGCTTCGACAGTGGGTGA 719

RESULT 13
ABQ73694
ID ABQ73694 standard; DNA; 720 BP.
XX
XX ABQ73694;
AC
XX
XX 07-OCT-2002 (first entry)
DT
XX
XX Humanised Renilla reniformis GFP nucleotide SEQ ID NO:3.
DE
XX
XX Renilla reniformis; green fluorescent protein; GFP; fluorescence;
XX fusion protein; intramolecular dimer; fluorescent protein; TOPP; FACS;
XX multimeric protein; fluorescence activated cell sorting; cell population;
XX viral vector infection; fluorescence resonance energy transfer; FRFT;
XX transgene expression; protein:protein interaction; humanised; gene; ds-.
XX
XX Renilla reniformis.
XX Homo sapiens.
XX Synthetic.
XX
XX Key location/Qualifiers
XX FH 1..720
XX CDS /*tag= a
XX FT /*product= "humanised green fluorescent protein"
XX FT /*transl_except= (pos:391..393,aa:Ser)
XX
XX WO200248174-A2.
```


CC also relates to sequences of the bioluminescence generating system
CC (e.g. luciferase). R. reniformis GFP are used in diagnostic methods
CC and in the production of novelty items such as toys (e.g. squirt gun,
CC pellet gun, toy "Halloween" eggs, toy cigarettes, board/card game
CC toys), finger paints, slimy play material, bubbles in bubble making
CC toys, fishing lures, dolls, sparklers, magic wand toys, balloons,
CC personal care item (e.g. cosmetic, bath powders, body creams, tooth
CC pastes, mouth wash, soaps, body paints, bubble bath), ornamental
CC transgenic plants, fountain, fairy dust, food (gelatins, icings,
CC frosting, beers, wine, champagne, milk, soft drinks, ice cubes, ice,
CC dry ice, beverage), textile (foot bag, clothing) and/or paper product
CC (greeting cards, wrapping paper). The present sequence is R. reniformis
CC GFP clone-2 DNA.
XX
XX
SO Sequence 860 BP; 298 A; 162 C; 175 G; 225 T; 0 other;

Query Match 23.4%; Score 257.8; DB 24; Length 860;
Best Local Similarity 62.0%; Pred. No. 4,4e-53;
Matches 425; Conservative 0; Mismatches 257; Indels 3; Gaps 1;

QY 55 AACACTGACGTGAAGAGATTATGTGGCAAAAGCTAGCGTTGACGAATCGTGAACAT 114
DB 65 AAACCTGTTGTTGAAGAGATGATGCTTAAATCACTTAGAAGAGCTGGTGGCGAC 128
QY 115 CACGTTTTTCATGGAAGATTTCGAAAGCATCTATTATTGGAACCAATTGATG 174
DB 129 CACGCTTCTCATATGGAAGAGATTGGCGAAGCAACATTTGGAAGAACTCAAGAGCTG 188
QY 175 CAAATCGGGTTACAAAGAGAGTCCGTTGCCATTCGTTTCATATTGTTCCATAGCT 224
DB 189 AAGATTCGTTAAACAAGAGCGGACGACCTCCATTCGATTCGATTCGATTCGTTGCT 248
QY 235 TTCCATATAGGGAATCGCACTTTCAGAAATACCCAGACACTTCGCGACTTCTTGT 294
DB 245 TTCTCATATGGAAGAGAGCTTATGTTCCGCAAGAAATTTCCAGTACTTCCCTC 308
QY 295 CAATCATTCGCCGCTGGATTCTTCTACGAAGAAATCTACGCTTGAAGATCGGCCATT 354
DB 309 CAGTCGTTTCCGAAGAGGCTTACTTACGAGAGAAACATTCGTTATCAAGATGAGAGACT 368
QY 355 GTTGACATTCGTTCAATATAGTTAGAAATGATGATAGCTCCACTACAAGTGAGATAT 414
DB 369 GCAATTGTTAAATCTGATATTAAGCTTGAAGATGTTAAATTCATAGTGAATGAGACTTC 428
QY 415 AGAGCGAATCGTTCCCTGTAACGAGCCCGATGACCAAAAGCCATCTCCGCAATGAG 474
DB 429 AAAGCGAAGGATCTAGCTGCAATGGAGCAGTCAATCCAGCAAGACATTCGTGGTATGCA 488
QY 475 CCATCGTTTGGAGTGGTCTACATGAACACCGCGCTTCGTTGGCGAAGTACATCTCGTT 534
DB 489 CCATCGTATGACTCAATGATGACACATGTCACCTTCATTATAGGSAATGTATATAGCA 548
QY 535 TACAAACGTCAGAGTCAAGGACTATTAAGTCTGCCACATGAAGAGTTTACAGATCCAAA 594
DB 549 TTCAAACCTTCAAACTGGCAAAACATTTCACTTACCAATGACGACAGCTTAAACAATCAAG 608
QY 595 GGTGAGTAAGAAATATCCCGGAATATCACTTATCCATCATCTGTTGGAAGAAACCTTAC 654
DB 609 AAGCCAGTGGAACTATGCACTATTGATTTCAATCCACATCGCTCTGTTGACCAAT 668
QY 655 GTGCA---AGAAGGAAGCTTCGTGGAACAAGAGAGCGCATTCACAACTGAGCACA 711
DB 665 GTGCAACAGCGCAGTGGTATGCTTGCAACAGAGACAGCAATTCGACGCACTTACGA 728
QY 712 ATTGAAAGCTCTGGGCTCCCTTC 736
DB 729 ATCAAAAATTAAGGCTCTTTTAC 753

RESULT 15
AAD22202
ID AAD22202 standard; DNA: 864 BP.
XX

AC AAD22202:
XX 12-FEB-2002 (first entry)
XX
XX
DE Renilla reniformis green fluorescent protein encoding DNA, clone-1.
XX
XX Green fluorescent protein; GFP; bioluminescence generating system; toy;
XX luciferase; finger paint; slimy play material; fishing lure; sparkler;
XX doll; balloon; personal care item; cosmetic; bath powder; body cream;
XX tooth paste; mouth wash; soap; body paint; ornamental transgenic plant;
XX bubble bath; fountain; fairy dust; food; gelatin; icing; frosting; beer;
XX wine; champagne; milk; soft drink; ice cube; ice; foot bag; beverage;
XX dry ice; textile; clothing; paper product; greeting card; wrapping paper;
XX sea pansy; ds.
XX
XX Renilla reniformis.
OS
XX
XX
XX Key Location/Qualifiers
FH 61..762
FT CDS
FT /ftag="a
FT /product="Renilla reniformis green fluorescent protein"

XX WO200168824-A2.
XX
XX
XX 20-SEP-2001.
XX
XX
XX 15-MAR-2001; 2001WO-US08277.
XX
XX
XX 15-MAR-2000; 2000US-189691P.
XX
XX
XX (PROL-) PROLUME LTD.
XX (BRYA/) BRYAN B. J.
XX
XX Bryan BJ, Szent-gyorgyi C, Szczepaniak W;
XX
XX WPI; 2002-010561/01.
XX P-PSDB; AAE13384.
XX
XX
XX Nucleic acids encoding Renilla reniformis green fluorescent proteins,
XX useful in diagnostic bioluminescence procedures -
XX
XX
XX Claim 3a: Page 164-165; 175pp; English.
XX
XX
XX The patent discloses sea pansy (Renilla reniformis) green fluorescent
XX proteins (GFP) and their corresponding polynucleotides. The invention
XX also relates to sequences of the bioluminescence generating system
XX (e.g. luciferase). R. reniformis GFP are used in diagnostic methods
XX and in the production of novelty items such as toys (e.g. squirt gun,
XX pellet gun, toy "Halloween" eggs, toy cigarettes, board/card game
XX toys), finger paints, slimy play material, bubbles in bubble making
XX toys, fishing lures, dolls, sparklers, magic wand toys, balloons,
XX personal care item (e.g. cosmetic, bath powders, body creams, tooth
XX pastes, mouth wash, soaps, body paints, bubble bath), ornamental
XX transgenic plants, fountain, fairy dust, food (gelatins, icings,
XX frosting, beers, wine, champagne, milk, soft drinks, ice cubes, ice,
XX dry ice, beverage), textile (foot bag, clothing) and/or paper product
XX (greeting cards, wrapping paper). The present sequence is R. reniformis
XX GFP clone-1 DNA.
XX
XX
SO Sequence 864 BP; 295 A; 164 C; 178 G; 227 T; 0 other;

Query Match 23.2%; Score 256.2; DB 24; Length 864;
Best Local Similarity 61.9%; Pred. No. 1.1e-52;
Matches 424; Conservative 0; Mismatches 258; Indels 3; Gaps 1;

QY 55 AACACTGACGTGAAGAGATTATGTGGCAAAAGCTAGCGTTGACGAATCGTGAACAT 114
DB 73 AAACCTGTTGTTGAAGAGATGATGCTTAAATCACTTAGAAGAGCTGGTGGCGAC 132
QY 115 CACGTTTTTCATGGAAGATTTCGAAAGCATCTATTATTGGAACCAATTGATG 174
DB 133 CACGCTTCTCATATGGAAGAGATTGGCGAAGCAACATATTGGAAGAGACTCAAGAGCTG 192

QY	175	CAAAATCCGGGTTACAAAAGGAGGTCGTTGCGCATTCGCTTTGCGAATATGTTTCCATAGCT	234
Db	193	AAGATATCGGAACAAAAGGCGACCACTCCCATTCGCATTGTATATCGATATCTGTGGCT	252
QY	235	TTTCCAAATACGGGAATTCGCACATTTTCCACAAATATCCCAACACACATTTGGGACTACTTTGTT	294
Db	253	TTTTTCATATGSGGAACAGAGCTTATACCGGTTATCCCAACAAATAATTCGCACTACTTCCTC	312
QY	295	CAATCATTTCCCGGCTGGATTTTCTACGAAGAATATCTACGCTTTGAGATGGCCCATTT	354
Db	313	CAGTCGTTTCCAGAAAGGCTTTACTTACGAAGAAACATTTGTTATCAAGATGAGGAACT	372
QY	355	GTTGACATTCCTTGAGATATATAGTTTGAAGATGATATAGTTTCCACTCAAGAGGAGTAT	414
Db	373	GCAATTTGTTAAATATGATATAGCTTTGGAAAGATGTAAATTTCAATGTAATGTAGACTTC	432
QY	415	AGAGGCAACGGTTTCCCTAGTAAACGAGACCCGTGATGCAAAAAGCCATCTCCGCGATGAG	474
Db	433	AAAGCAAGAGATCTACGTCGCGATGGGACACAGTATATGCAAGAACATCGTGGGTTATGCA	492
QY	475	CCATTCGTTTGAAGTGTCATCATGAACAGCGGGCTTCTGCTGGGCGAAGTATCTTCGTT	534
Db	493	CCATTCGTATGATCAATGATACACCAATAGTCACTTCACTTTTAGGGCAATGTATAATAGCA	552
QY	535	TACAAACTCGATGAGGAACTATTATCTCGGCCACATGAAACGTTTACATACCAAA	594
Db	553	TTTCAAACTTCAAACTGTGGACAACTTTACTTACCCATGAGACAGTTTATCAAAATCAAAG	612
QY	595	GGTGAGAGTAAAGAAATTCGCCGAATATCACATTATCCATCATGATGCTCGAGAAACCTAC	654
Db	613	AAGCAGATGGAACCTATGCCATTGTATCATTTTCAATCCAGAGCATGGCCGTTAAGACCAAT	672
QY	655	GTGGA---AGAGAAGCTTGTGGAACAACAGAGACGGCCATTGCAACAATGACACCACA	711
Db	673	GTGGAACAACAGCCACTGTGTAGCTGTGCAACACAGAGACCAAAATTTGACGGCATCTTACA	732
QY	712	ATTGGAAAACCTCTGGGCTCCCTTC	736
Db	733	ATCAAAAAAATTGAAGGCTCTTTAG	757

Search completed: January 16, 2003, 12:20:04
Job time : 277.506 secs

GenCore version 5.1.3
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OH nucleic - nucleic search, using sw model

Run on: January 16, 2003, 11:05:09 ; Search time 1815.57 Seconds
(without alignments)
9842.636 Million cell updates/sec

Title: US-09-710-058A-3
Perfect score: 1104
Sequence: 1 tcgcgcagcgtgcctcca.....caaaaaaaaaaaaaaa 1104

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estlin:*
16: em_estlom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	5.2	470	13	BM275720 PESTroa5
2	53.4	4.8	1101	17	CNS0039G AL063921 Drosophi1
3	50	4.5	1101	17	CNS000YWL AL066927 Drosophi1
4	49.8	4.5	252	9	AU262806 AU262806
5	49.2	4.5	147	17	DR13H8T AL740356 Danio rer
6	49.2	4.5	369	5	AL515019 AL515019

Result	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	BM275720	470 bp mRNA linear EST 20-DEC-2001	BM275720	1	PIESTroa56f06.y1 Plasmodium falciparum 3D7 gametocyte cDNA library	Plasmodium falciparum 3D7	Plasmodium falciparum 3D7	1 (bases 1 to 470)	Tang,K., Cole,R., Chakrabarti,D., Haywood,R., Clifton,S., Pape,D., Marra,M., Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B., Bowers,Y., Gibbons,M., Ritten,E., Bennett,J., Jones,E., Ronko,I., Tsagarelisvili,R., Belaygorod,L., Franklin,C., Carr,L., Grow,A., Maquire,L., Richey,J., Wadkin,J., Kennedy,S., Levinso,D., Wareston,R., Wilson,R. and Sibley,D.	Washu Plasmodium EST Project	Unpublished (2001)	Contact: L. David Sibley Washu Plasmodium EST Project Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Library was constructed by R. Haywood. DNA sequencing by:

ALIGNMENTS

The BDGP is constructing a physical map of the *Drosophila melanogaster* genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP *Drosophila melanogaster* BAC library was prepared by Kazuhiro Oseegawa and Aaron Mammeter in Pierer de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPc1-98 and was constructed by partial EcoRI digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library

ONOMASTIC PHILOSOPHY OF METAPHYSICS

REFERENCE	AUTHORS	TITLE	JOURNAL
1	(bases 1 to 1101)	Genoscope.	
2	Direct Submission		
3	Submitted (23-JUL-1999)	Genoscope - Centre National de Séquençage	
4	BP 191 91005 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr		
5	Web : www.genoscope.cns.fr		
6	Determination of this BAC-end sequence was carried out as part of a		
7	collaboration with the European Drosophila Genome Project (EDGP) -		
8	http://www.edgp.abl.ac.uk - This Drosophila melanogaster BAC		
9	library (Dros BAC) was made by Alain Rillaud at CPFH (Centre		
10	d'Etude du Polymorphisme Humain) with funding provided by a MRC		
11	project grant. The DNA was prepared from embryos by Alain Bucheton		
12	and Genevieve Payan. It has been constructed in the vector		
13	phe10BAC11.		
FEATURES	source	Location/Qualifiers	
		1..1101	
		/organism="Drosophila melanogaster"	
		/db_xref="taxon:7227"	
		/clone="BACN01G13"	
		/clone_id="DrosBAC"	
		/plasmid="phe10BAC11"	
		/note="end : SP6"	
BASE COUNT	424 a	119 c	129 g 248 t 181 others
ORIGIN			
Query Match	4.5%	Score 50:	DB 17: Length 1101:
Best Local Similarity	38.4%	Pred. No. 9.6:	
Matches	84: Conservative	38: Mismatches	97: Indels 0: Gaps 0:
QY	886	AAAGCAACCTCGAAGCATTTGAAACCTCGAAGCATATTGAAACCTCGACGAGACCGT	945
Db	812	WAAAAAATAATATATWAAATATAAAAAATAAAAKAMNATWTTATAAAAAAATAATAAT	871
QY	946	AAAGACCCGCAAAATTAACCCCTTCACACGACAGTTGCAATCTTTAAACCGATCAAA	1005
Db	872	AARWTAATAAAAAAAMAMAMATMAATATATATWMAAAAAAATTTAAWMAAMTAAWAK	931
QY	1006	ACTATTATATATATATATATATACCTGTATATACCTATATATATATATATATATATAT	1065
Db	932	ATAAAAAAMAAAAARNAATATAMAAAAATWMTATAMATMTATATATATATATATATTA	991
QY	1066	GATTAAATCTGCTTGTGATCAAAAAAAAAAAAAAAAAAAAAA	1104
Db	992	TADTWATANTMAATKTAMDWAMATATATAMWAMAMAAAA	1030
RESULT 4			
LOCUS	AU262806	252 bp	mrna linear EST 09-MAY-2002
DEFINITION	AU262806 VS Dictyostelium discoideum cDNA clone VSC810 3', mRNA		
ACCESSION	AU262806		
VERSION	AU262806.1	GI:20519353	
KEYWORDS	EST.		
SOURCE	Dictyostelium discoideum.		
ORGANISM	Dictyostelium discoideum		
REFERENCE	1 (bases 1 to 252)		
AUTHORS	Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochial,H., Meeda,M.,		
TITLE	Takeuchi,I., Kohara,Y. and Tanaka,Y.		
JOURNAL	Population analysis of cDNAs from unicellular and multicellular		
COMMENT	stages of Dictyostelium discoideum		
	Unpublished (2002)		
	Contact: Hideko Urushihara		
	Institute of Biological Sciences		
	University of Tsukuba		
	1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan		
	Tel: 81-298-53-4664		
	Fax: 81-298-53-6614		
	Email: hideko@biol.tsukuba.ac.jp.		

FEATURES					
Source		location/Qualifiers			
		1..252			/organism="Dictyostelium discoideum"
					/strain="AX4"
					/db_xref="taxon:44689"
					/clone="VSC810"
					/clone_1id="VS"
					/sex="mat A"
					/dev_stage="vegetative"
BASE COUNT	145 a	19 c	14 g	74 t	
ORIGIN					
Query Match	4.5%:	Score 49.8:	DB 9:	Length 252:	
Best Local Similarity	68.3%:	Pred. No. 17:	Mismatches 32:	Indels 0:	Gaps 0:
Matches 69:	Conservative 0:	Mismatches 32:	Indels 0:	Gaps 0:	
OY	1004	AAACATTATTAATTAATTAATACCCTGATAACTTATATATATCATGTGGATA	1063		
Db	150	ATACCCATAAATATTTATATCTAAATATATAAATCTTATATATATTTATATTACA	209		
OY	1064	TTGATTAAATCTGTTCTTGATCAAAAAAAAAAAAAAAA	1104		
Db	210	CTTAATAATTAATTAATTAATAAAAAAAAAAAAAAGA	250		
RESULT 5					
DRI3H8T/C		147 bp	DNA	linear	GSS 06-JUN-2002
LOCUS	Danio rerio genomic clone DKey-13H8,				genomic survey sequence.
DEFINITION	AL740366				
ACCESSION	AL740366.1	GI:21338729			
VERSION	GSS.				
KEYWORDS	zebrafish.				
SOURCE	Danio rerio				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Actinopterygii; Neopterygii; Teleostei; Ostraciophysi;				
	Cypriniformes; Cyprinidae; Danio.				
REFERENCE	1 (bases 1 to 147)				
AUTHORS	Humphray, S.J., Huckle, E. and Hunt, S.E.				
TITLE	Direct Submission				
JOURNAL	Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humphr@sanger.ac.uk Unpublished				
	This sequence was generated from the T7 end of BAC 13H8. 13H8 is part of the Daniokey Pilot BAC Library created by R. Plasterk and N.V. Keyene.				
COMMENT	Further details: http://www.sanger.ac.uk/Projects/D_rerio/.				
FEATURES					
Source		Location/Qualifiers			
		1..147			/organism="Danio rerio"
					/db_xref="taxon:7955"
					/clone="DKey-13H8"
					/tissue-type="Testis"
					/note="vector pindigobAC-536"
BASE COUNT	53 a	7 c	7 g	80 t	
ORIGIN					
Query Match	4.5%:	Score 49.2:	DB 17:	Length 147:	
Best Local Similarity	67.6%:	Pred. No. 26:	Mismatches 33:	Indels 0:	Gaps 0:
Matches 69:	Conservative 0:	Mismatches 33:	Indels 0:	Gaps 0:	
OY	1003	AAACCTATTAAATFAAATATFATACCTGTAGTAACCTATATATATATATATAGTTGAT	1062		
Db	142	ATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT	83		
OY	1063	ATTGATTAAATCTGTTCTTGATCAAAAAAAAAAAAAAAA	1104		
Db	82	ATTATATAAATTTGATTTTTGAACAAAAAACAAAAACAA	41		
RESULT 6					
LOCUS	AL515019	369 bp	mRNA	linear	EST 13-FEB-2001

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DEFINITION      AL515019 LTL.NFL006.PL2 Homo sapiens cDNA clone CL0BB0262B06 3
prime, mRNA sequence.
ACCESSION       AL515019
VERSION         AL515019.1 GI:12778512
KEYWORDS        EST.
SOURCE          human.
ORGANISM        Homo sapiens
                 Chordata; Craniata; Vertebrata; Euteleostomi;
                 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE       1 (bases 1 to 369)
AUTHORS         Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE           Full-length cDNA libraries and normalization
JOURNAL         Unpublished (2001)
COMMENT         Contact: Genoscope
                 Genoscope - Centre National de Sequencage
                 BP 191 91006 Evry cedex - France
                 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES        source
                 1..369
                 /organism="Homo sapiens"
                 /db_xref="taxon:9606"
                 /clone_id="LTL.NFL006.PL2"
                 /tissue_type="placenta"
                 /note="Vector: pCMVSPORT 6; Site:1: NotI; 1st strand cDNA
                 was primed with a NotI-Oligo(dT) primer. Five prime end
                 enriched, double-stranded cDNA was digested with Not I and
                 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                 vector. Library was normalized. Library was constructed by
                 Life Technologies. Contact : Feng Liang Life Technologies,
                 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                 Email : fliang@lifetech.com URL :
                 http://fulllength.invitrogen.com"
BASE COUNT      156 a 7 c 2 g 179 t 25 others
ORIGIN
Query Match      4.5%; Score 49.2; DB 9; Length 369;
Best Local Similarity 44.4%; Pred. No. 19;
Matches 138; Conservative 5; Mismatches 168; Indels 0; Gaps 0;
OY 794 TTGTGTATACAAATATTTGGGTCATTTTGAATGCTATGCTGTGTATGATCATATA 853
DB 1111111111111111111111111111111111111111111111111111111111
OY 58 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 117
DB 854 GACGTCGTCATCATAGCTGATGATCCTTCAGCAAAAGAAACCTCGAAGCATTTGAACC 913
OY 118 TKTTRNNNTTTANNNTNNTTNNNTTANNNTTAAAAAAATTAATAAAATTAAC 177
DB 914 TCGAAGCATATTGAACCTCGACGAGAGCGTAAGAGACCGACAATTAACGGCTTTC 973
OY 178 AATTAAATATATATTAATAAAATAAAATAAAATAAAATAAAATAAANTTAATATWTA 237
DB 974 AACGACAGTGGAACTTTTAAACGATCAAAAGTAATTAATATATATATACCTGT 1033
OY 238 WAAAAAATATATATATATTAATAAAATAAAATAAAATAAAATAATTTTATATATATAT 297
DB 1034 ATAACTTATATATATATATATATGTTGATGATTAATTCGTCTGATCAAAAAA 1093
OY 298 ATAAATATATATATATATATATATATATATATATATATATATATATATATATAT 357
DB 1094 AAAAAAAAAA 1104
OY 358 AAAAAAAAAA 368

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VERSION          AL103735.1 GI:5615346
KEYWORDS         GSS.
SOURCE           Drosophila melanogaster.
ORGANISM         Drosophila melanogaster
                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                 Ephydroidea; Drosophilidae; Drosophila.
REFERENCE        1 (bases 1 to 1043)
AUTHORS          Direct Submission
TITLE            Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage ;
JOURNAL          BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
COMMENT          - Web : www.genoscope.cns.fr)
                 Determination of this BAC-end sequence was carried out as part of a
                 collaboration with the European Drosophila Genome Project (EDGP) -
                 http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
                 library (Dros BAC) was made by Alain Billaud at CEPH (Centre
                 d'Etude du Polymorphisme Humain) with funding provided by a MRC
                 project grant. The DNA was prepared from embryos by Alain Bucheton
                 and Genevieve Payan. It has been constructed in the vector
                 pBelobAC11.
FEATURES        Location/Qualifiers
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                 /organism="Drosophila melanogaster"
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                 /clone_lib="DrosBAC"
                 /plasmid="pBelobAC11"
                 /note="end : T7"
BASE COUNT       277 a 96 c 121 g 382 t 167 others
ORIGIN
Query Match      4.5%; Score 49.2; DB 17; Length 1043;
Best Local Similarity 37.5%; Pred. No. 14;
Matches 105; Conservative 40; Mismatches 135; Indels 0; Gaps 0;
OY 825 TAATGTATATGTTGTGTATGATCAATAGACGTCGATTCATATGCTTGAATCCTTAG 884
DB 1111111111111111111111111111111111111111111111111111111111
OY 845 TTWTWTWMMWMMWMTTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWT 756
DB 885 CAAAAGAAACCTCGAAGCATATTTGAACCTCGAAGCATATTTGAACCTCGAGGAGCG 944
OY 755 AAAAAAANATNTWAAATATATATTAATTAAMWATWATWATATATATATATATAT 696
DB 945 TAAAGACCGCAACAATTAACGCTTTCACACAGTGTGAATCTTAAACCGATCAA 1004
OY 695 TTATWAMWAMWATATATTAAMWAMWAMWAMWAMWAMWAMWATATATTTWMMWATAAW 636
DB 1005 AACTATTAATTAATATATATATACCTGTATATATATATATATATATATATAT 1064
OY 635 AAMWMAAAAAAAMWATATATATATTTWTTWATATATATATATATATATATATAT 576
DB 1065 TGATTAATCTGTCTTCTGATCAAAAAAATAAAAAAATAAAAAA 1104
OY 575 TAMATWMTATWATATATATATATATATATATATATATATATATATATATATAT 536
DB 575 TAMATWMTATWATATATATATATATATATATATATATATATATATATATATAT

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RESULT 8
LOCUS      BM358135          945 bp      mRNA      linear      EST 09-JAN-2002
DEFINITION GA_Ea0005115r Gossypium arboreum 7-10 dpa fiber library Gossypium
ACCESSION  BM358135
VERSION    BM358135
KEYWORDS   Gossypium arboreum.
SOURCE     Gossypium arboreum
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eustosids II; Malvales; Malvaceae; Gossypium.
REFERENCE  1 (bases 1 to 945)
AUTHORS    Wing,R.A., Fritsch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry
            ,D., Wood,T.C., Leslie,A. and Wilkins,T.A.

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source
1. .109
/organism="Dictyostelium discoideum"
/strain="AX4"
/cd_xref="taxon:44689"
/cd_name="ddv55c11"
/clone_1id="Dictyostelium discoideum cDNA library, VF"
/sex="mat A"
/dev_stage="growth phase"

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ORIGIN

Query Match      4.4%: Score 48.2; DB 13; Length 109;
Best Local Similarity 64.8%: Pident.No. 44;
Matches 68; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

OY 1000 ATCAAACTATTATATATATATATACCCGTCTTAAGTATATATATATAGTTT 1059
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2 ATAAATACATTATTATGTATAATAATATATATATATATATATATATATATATA 61

OY 1060 GATATGATTAATCTGTTGATCAAAAAAAAAAAAAAAAAAAAA 1104
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 62 AACATTTTTTTTTTTTTTTTNNGTTTAAAAAATAATNAAAAA 106

RESULT 11
LOCUS      CNS00FTW      1101 bp      DNA      linear      GSS 04-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC:
            BACR29L17 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION  AL069847
VERSION     AL069847.1 GI:4949799
KEYWORDS   GSS.
ORGANISM   Drosophila melanogaster.
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 1101)
            Genoscope.
            Direct Submission
            Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
            Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mamoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
            Location/Qualifiers
            1. .1101
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               /db_xref="taxon:7227"
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               /note="end : TET3"

BASE COUNT      181 a      172 c      126 g      351 t      271 others
ORIGIN

Query Match      4.3%: Score 40.2; DB 17; Length 1101;
Best Local Similarity 38.0%: Pident.No. 22;
Matches 92; Conservative 39; Mismatches 111; Indels 0; Gaps 0;

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OY		858	TGCGATCTTCAGACTTGACCTTCCAGCAAAAGAACCCTCACAACCATATTGAACCTTCGA	917
Dd		975	TCYCMACAAAMWMTCTCAHTYYWWYCAAMAATAAATAATTATTTCTAMAWAAAAANANA	916
OY		918	AGCATATTGGAAACCTCGACGAGAGCCGTAAAAGACGCCACAAATTAACGC GTTCAAC C	977
Dd		915	AAATTTATWTAACTTMWAAMAAAMMMMAAMMWAMVTMMMAAATATCTTAMMMAAAAT	856
OY		978	AGCAGTTGGATCTTTTTAACCGATCAACACATTTATTAATATATATACCCTGTATAA	1037
Dd		855	AMAAAAATTTTANMANAMAVTTTWAAAAANAMANAAAAAAAAAAATAABAAAAAAA	796
OY		1038	CTTATATATATCTATAGTAGTTGATFTTGGATTTAAATCTGTTGGATCAAAAAA	1097
Dd		795	AAATATATACATAMMAAAVATTTATWMMAAAAAAMMAAAAMATTTATMAAAMAAAAA	736
OY		1098	AA 1099 Dd 735 AA 734	
RESULT#	12	CNS02MEY	761 bp DNA linear GSS 14-MAY-2000	
LOCUS		Locus		
DEFINITION		Tetradodon nigroviridis genome survey sequence PUC-Ori end of clone		
FEATURES		149E02 of library G from Tetradodon nigroviridis, genomic survey		
VERSION		AL204019		
KEYWORDS		AI204019.1 GI:7862838		
SOURCE		GSS; genome survey sequence.		
ORGANISM		Tetradodon nigroviridis. Tetradodon nigroviridis. Tetradodon nigroviridis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acantthonomidae; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetraodontidae; Tetraodon. 1 (bases 1 to 761) Roest-Crollius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher.C, Bernot,A., Fizames.C., Winkler,P., Brotlier.P., Quetier.F., Saurin,W. and Weissenbach,J. Human gene number estimate provided by genome wide analysis using Tetradodon nigroviridis DNA sequence Unpublished 2 (bases 1 to 761) Roest-Crollius,H., Jalllon,O., Dasilva,C., Fizames.C., Fisher.C., Bouneau.L., Billault.A., Quetier.F., Saurin,W., Bernot,A. and Weissenbach.J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis unpublished 3 (bases 1 to 761) Genoscope. Direct Submission Submitted (12-APR-2000)		
JOURNAL REFERENCE		This sequence is a single read and was generated as part of a large scale clone-and-sequencing project of the Tetradodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetradon.		
JOURNAL AUTHORS		Location/Qualifiers		
TITLE		1..761		
JOURNAL REFERENCE		/organism="Tetradodon nigroviridis"		
AUTHORS		/db_xref=taxon:99883"		
TITLE		/clone_1id= "149E02"		
JOURNAL COMMENT		/clone_lid="G"		
FEATURES		/note="Genoscope sequence ID : COAG149BCO1sp1-end :		
SOURCE		PUC-Ori"		
BASE COUNT		221 a 116 c 73 g 245 t 106 others		
ORIGIN				
Query Match		4.3% ; Score 47.8; DB 17;	length 761;	
Best Local Similarity		57.3%; Pred No.28;		
Matches		59; Conservative	13; Mismatches	31; Indels 0; Gaps 0;

[illegible][illegible]

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 16, 2003, 08:03:43 : Search time 49.0554 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
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Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1104	100.0	1104	US-09-277-716-30	Sequence 30, Appl
2	1104	100.0	1104	US-09-609-161B-30	Sequence 30, Appl
3	760.2	68.5	1275	US-09-277-716-31	Sequence 31, Appl
4	760.2	68.5	1275	US-09-609-161B-31	Sequence 31, Appl
5	394.2	35.7	1079	US-09-609-161B-15	Sequence 15, Appl
6	394.2	35.7	1085	US-09-277-716-15	Sequence 15, Appl
7	160	14.5	801	US-09-459-956-7	Sequence 7, Appl
8	132.4	12.0	678	US-09-459-956-6	Sequence 6, Appl
9	132.2	12.0	659	US-09-459-956-5	Sequence 5, Appl
10	111.2	10.1	650	US-09-459-956-2	Sequence 2, Appl
11	94.6	8.6	695	US-09-459-956-3	Sequence 3, Appl
12	93	8.4	656	US-09-459-956-4	Sequence 4, Appl
13	40.2	3.6	789	5219739-8	Patent No. 5219739
14	40	3.6	5852	US-07-867-106-2	Sequence 2, Appl
15	39.4	3.6	790	5194596-8	Patent No. 5194596
16	39.4	3.6	1117	US-09-247-373B-13	Sequence 33, Appl
17	39.2	3.6	2108	US-08-700-745A-6	Sequence 6, Appl
18	39.2	3.6	2108	US-09-020-684-6	Sequence 6, Appl
19	39.2	3.6	2108	US-09-020-467-6	Sequence 5, Appl
20	39.2	3.6	2108	US-09-020-685-6	Sequence 6, Appl
21	38.8	3.5	2277	US-09-020-683-6	Sequence 6, Appl
22	38.8	3.5	2277	US-08-676-967-2	Sequence 2, Appl
23	38.8	3.5	2277	US-08-676-974-2	Sequence 2, Appl
24	38.8	3.5	2277	US-09-098-487-2	Sequence 2, Appl
25	38.6	3.5	1890	5312912-3	Patent No. 5312912
26	38.6	3.5	6038	US-09-305-639-4	Sequence 4, Appl
27	38.6	3.5	7622	US-09-305-639-1	Sequence 1, Appl

C 28	38.4	3.5	8920	2	US-08-446-855A-1	Sequence 1, Appl
C 29	38.4	3.5	8920	4	US-09-150-741-1	Sequence 1, Appl
30	38	3.4	944	1	US-08-452-295-2	Sequence 2, Appl
31	38	3.4	961	6	5194596-16	Patent No. 5194596
32	38	3.4	961	6	5219739-16	Patent No. 5219739
33	38	3.4	961	6	5219739-16	Patent No. 5219739
C 34	38	3.4	17949	4	US-09-087-465-3	Sequence 1, Appl
C 35	37.8	3.4	7257	3	US-08-817-926-27	Sequence 27, Appl
C 36	37.6	3.4	4818	3	US-08-232-463-14	Sequence 14, Appl
C 37	37.2	3.4	7218	1	US-08-451-405A-2	Sequence 2, Appl
38	37.2	3.4	731	1	US-09-029-213B-7	Sequence 7, Appl
39	36.8	3.3	8920	2	US-08-446-855A-1	Sequence 1, Appl
40	36.8	3.3	8920	4	US-09-150-741-1	Sequence 1, Appl
41	36.6	3.3	8585	1	US-08-030-096-3	Sequence 3, Appl
42	36.6	3.3	51952	3	US-08-947-823-1	Sequence 1, Appl
43	36.4	3.3	714	3	US-09-172-063-15	Sequence 15, Appl
44	36.4	3.3	714	3	US-09-172-063-16	Sequence 16, Appl
45	36.4	3.3	714	4	US-09-316-919-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-277-716-30
; Sequence 30, Application US/09277716A
; Patent No. 6232107
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; APPLICANT: Szent-Gyorgyi, Christopher
; APPLICANT: PROLUME, LTD.
; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
; CURRENT APPLICATION NUMBER: US/09/277,716A
; EARLIER FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 60/102,939
; EARLIER FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: 60/089,367
; EARLIER FILING DATE: 1998-06-15
; EARLIER APPLICATION NUMBER: 60/079,624
; EARLIER FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 1104
; TYPE: DNA
; ORGANISM: Ptilosarcus gurneyi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)..(747)
; FEATURE:
; OTHER INFORMATION: Ptilosarcus Green Fluorescent Protein (GFP) (insert A)
US-09-277-716-30

Query Match 100.0% Score 1104; DB 4; Length 1104;
Best local similarity 100.0% Pred. No. 9.5e+255;
Matches 1104: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TCGGCAGCAGCTGGCCCTCCACACTTTAGACAAATGACCGGCAACGTATTAAAGAACT	60
DB	1	TCGGCAGCAGCTGGCCCTCCACACTTTAGACAAATGACCGGCAACGTATTAAAGAACT	60
QY	61	GGACGTGAAGACATATATGTCGGCAAAAGTACGTTGAAGGAATGCTGACAATCAGCTT	120
DB	61	GGACGTGAAGACATATATGTCGGCAAAAGTACGTTGAAGGAATGCTGACAATCAGCTT	120
QY	121	TTTTCATGAGAGATTTGGAAGCAATGATTTGGAACCAATTTGATGCAATC	180
DB	121	TTTTCATGAGAGATTTGGAAGCAATGATTTGGAACCAATTTGATGCAATC	180
QY	181	CGGCTTACAAAGGAGGTCGTTGCCATTGCTTTGCATATGTTCCATACCTTTCCAA	240
DB	181	CGGCTTACAAAGGAGGTCGTTGCCATTGCTTTGCATATGTTCCATACCTTTCCAA	240

Oy	241	TACGGAAATGCGACTTTTACGAAATACCCAGACGACATTTGGGACTACTTTGTTCAATCA	300
Dp	241	TACGGAAATGCGACTTTTACGAAATACCCAGACGACATTTGGGACTACTTTGTTCAATCA	300
Oy	301	TTCCCGGCGTGAATTTTCTACGAAAGAATCTACGCTTTGAAAGTGGGCGATTGTTTAC	360
Dp	301	TTCCCGGCGTGAATTTTCTACGAAAGAATCTACGCTTTGAAAGTGGGCGATTGTTTAC	360
Oy	361	ATTGCTTCAGATATATAGTTTATAGAAAGATATAGTTCCACTCAAAAGTGGAGTATAGAGC	420
Dp	361	ATTGCTTCAGATATATAGTTTATAGAAAGATATAGTTCCACTCAAAAGTGGAGTATAGAGC	420
Oy	421	AACGGTTTCCCTAGTAAACGAGCCGCTGATGCAAAAAGCCATCTCCTGCGATGAGCGATCG	480
Dp	421	AACGGTTTCCCTAGTAAACGAGCCGCTGATGCAAAAAGCCATCTCCTGCGATGAGCGATCG	480
Oy	481	TTTGAAGTGGTCTACATGAAAGCGCGCTCTGTGGGCGAAGATAGATCTGTTTACAA	540
Dp	481	TTTGAAGTGGTCTACATGAAAGCGCGCTCTGTGGGCGAAGATAGATCTGTTTACAA	540
Oy	541	CTCGGTGAGGGAACATATTACTCGTCCGCCACATGMAAACGTTTTACAGATCCAAAGTGTGA	600
Dp	541	CTCGGTGAGGGAACATATTACTCGTCCGCCACATGMAAACGTTTTACAGATCCAAAGTGTGA	600
Oy	601	GTGAAGAATTTCCCGGAATATCTACTTTATCCATCATCTCTGTGAGAAACCTACGTTGAA	660
Dp	601	GTGAAGAATTTCCCGGAATATCTACTTTATCCATCATCTCTGTGAGAAACCTACGTTGAA	660
Oy	661	GAAGAACTCTGTGTGAACAACACGAGCGCCATTTGACAACTGTACCAATTTGGAAAA	720
Dp	661	GAAGAACTCTGTGTGAACAACACGAGCGCCATTTGACAACTGTACCAATTTGGAAAA	720
Oy	721	CCTCTGGGCTCCCTTCATGAATGCGGTAGAAAAATGACCAATATCTGGGGAACCGATA	780
Dp	721	CCTCTGGGCTCCCTTCATGAATGCGGTAGAAAAATGACCAATATCTGGGGAACCGATA	780
Oy	781	ACCGTTTGAAGCTTGCTATACAAATTTATTTGGGGCTATTTGTAATGTATGTGTGT	840
Dp	781	ACCGTTTGAAGCTTGCTATACAAATTTATTTGGGGCTATTTGTAATGTATGTGTGT	840
Oy	841	TGTATGATCAATAGACGTCGTCATTCATAGCTTGAACTTCAGCAAAAGAAACCTCGAA	900
Dp	841	TGTATGATCAATAGACGTCGTCATTCATAGCTTGAACTTCAGCAAAAGAAACCTCGAA	900
Oy	901	GCATATTGAAACCTCGAGACGATATTGAAACCTCGAGCGAGAGCGTAAAGAGACCGCACAA	960
Dp	901	GCATATTGAAACCTCGAGACGATATTGAAACCTCGAGCGAGAGCGTAAAGAGACCGCACAA	960
Oy	961	ATTAAACGGCTTCAACCGACGAGCTTGGAATCTTTTAAACCGATCAAAACATTAATTAAT	1020
Dp	961	ATTAAACGGCTTCAACCGACGAGCTTGGAATCTTTTAAACCGATCAAAACATTAATTAAT	1020
Oy	1021	ATATATACCCCTGTATACCTTTATATATCTATATAGTTGATATGATTAATCTGTCT	1080
Dp	1021	ATATATACCCCTGTATATCTTATATATCTATATAGTTGATATGATTAATCTGTCT	1080
Oy	1081	TGATCAAAAAAAAAAAAAAAAAAAAA 1104	
Dp	1081	TGATCAAAAAAAAAAAAAAAAAAAAA 1104	

RESULT 2
 US-09-609-161B-30
 ; Sequence 30, Application US/09609161B
 ; Patent No. 6436682
 ; GENERAL INFORMATION:
 ; APPLICANT: Bryan, Bruce
 ; APPLICANT: Szent-Gyorgyi, Christopher
 ; APPLICANT: PROLUME, LTD
 ; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUCIFERASES, AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGH-THROUGHPUT SCREENING AND NOVELTY ITEMS
 ; TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
 ; FILE REFERENCE: 24729-121B

	Query Match	Best Local	Similarity	Score	1104:	DB	4:	Length	1104:
	Matches	1104:	Conservative	0:	Mismatches	0:	Indels	0:	Gaps
0Y	1	TCGGACGACGCTGGCCCTCCACACTTTAGACAAATAAGACCGCACGTAATTAAGAACA	100.0%	100.0%	DB	4:	Length	1104:	
Db	1	TCGGACGACGCTGGCCCTCCACACTTTAGACAAATAAGACCGCACGTAATTAAGAACA	100.0%	100.0%	DB	4:	Length	1104:	
0Y	61	GGACTGAAAGACATTTATGTCGGCAAAAGCTAGCGTTTGAAAGATGCTGACATACGTT	100.0%	100.0%	DB	4:	Length	1104:	
Db	61	GGACTGAAAGACATTTATGTCGGCAAAAGCTAGCGTTTGAAAGATGCTGACATACGTT	100.0%	100.0%	DB	4:	Length	1104:	
0Y	121	TTTTCCATGGAAGGATTTGGAAAGCAATGATATTGTTGGAACCAATGATGCAATTC	100.0%	100.0%	DB	4:	Length	1104:	
Db	121	TTTTCCATGGAAGGATTTGGAAAGCAATGATATTGTTGGAACCAATGATGCAATTC	100.0%	100.0%	DB	4:	Length	1104:	
0Y	181	CGGGTTACAAAGGAGGCGCTTGGCATTCGCTTGCATATTGTTCCATAGCTTCCAA	100.0%	100.0%	DB	4:	Length	1104:	
Db	181	CGGGTTACAAAGGAGGCGCTTGGCATTCGCTTGCATATTGTTCCATAGCTTCCAA	100.0%	100.0%	DB	4:	Length	1104:	
0Y	241	TACGGGAATCGACATTTACGAATAACCCAGACATTTGGCGACTACTTTGTCAATCA	100.0%	100.0%	DB	4:	Length	1104:	
Db	241	TACGGGAATCGACATTTACGAATAACCCAGACATTTGGCGACTACTTTGTCAATCA	100.0%	100.0%	DB	4:	Length	1104:	
0Y	301	TTCCCGGCTGGAATTTTCTACGAAGAATCTACGCTTTGAAGATGGCGCCATTTGTAC	100.0%	100.0%	DB	4:	Length	1104:	
Db	301	TTCCCGGCTGGAATTTTCTACGAAGAATCTACGCTTTGAAGATGGCGCCATTTGTAC	100.0%	100.0%	DB	4:	Length	1104:	
0Y	361	ATTCCGTCGATATATAGTTTAGAAGATGATAGTTCCACTACAAAGTGAGATAGAGGC	100.0%	100.0%	DB	4:	Length	1104:	
Db	361	ATTCCGTCGATATATAGTTTAGAAGATGATAGTTCCACTACAAAGTGAGATAGAGGC	100.0%	100.0%	DB	4:	Length	1104:	
0Y	421	AACGGTTTCCATGATTAACGAGACCCGATGATGCAAAAGCCATCTCGGCATGAGCCATCG	100.0%	100.0%	DB	4:	Length	1104:	
Db	421	AACGGTTTCCATGATTAACGAGACCCGATGATGCAAAAGCCATCTCGGCATGAGCCATCG	100.0%	100.0%	DB	4:	Length	1104:	
0Y	481	TTTTGAGGTGCTACATATGAACAGCGCGCTTCTGCTGGGGGAAGTAGATCTGTTTACAA	100.0%	100.0%	DB	4:	Length	1104:	
Db	481	TTTTGAGGTGCTACATATGAACAGCGCGCTTCTGCTGGGGGAAGTAGATCTGTTTACAA	100.0%	100.0%	DB	4:	Length	1104:	
0Y	541	CTCGAGTCGAGGAACATTTACTCTGTCGACATGAAACGTTTTACAGATCCAAAGGTGA	100.0%	100.0%	DB	4:	Length	1104:	
Db	541	CTCGAGTCGAGGAACATTTACTCTGTCGACATGAAACGTTTTACAGATCCAAAGGTGA	100.0%	100.0%	DB	4:	Length	1104:	
0Y	601	GTTGAAGAATTTCCCGGAATATCATTTATCATCATCTGTTGAGAGAAAACCTACGTGAA	100.0%	100.0%	DB	4:	Length	1104:	
Db	601	GTTGAAGAATTTCCCGGAATATCATTTATCATCATCTGTTGAGAGAAAACCTACGTGAA	100.0%	100.0%	DB	4:	Length	1104:	
0Y	661	GAAGGAAGCTTCTGAGAACACAGAGAGCGCATATGACAACTGACCAATTTGGAAAA	100.0%	100.0%	DB	4:	Length	1104:	
Db	661	GAAGGAAGCTTCTGAGAACACAGAGAGCGCATATGACAACTGACCAATTTGGAAAA	100.0%	100.0%	DB	4:	Length	1104:	

QY 721 CCTCTGGGCTCCCTTCATGATGCGTGTAGAAAAATGACCAATATAGTGGGAAACCGATA 780
|||||
Db 721 CCTCTGGGCTCCCTTCATGATGCGTGTAGAAAAATGACCAATATAGTGGGAAACCGATA 780
QY 781 ACCGTTTGGAGACCTTGTGTATACAAATTTTGGGCTCATTTTGTAAATGTGTATGTGT 840
|||||
Db 781 ACCGTTTGGAGACCTTGTGTATACAAATTTTGGGCTCATTTTGTAAATGTGTATGTGT 840
QY 841 TGTATGATCATATAGACGTGTCTCATTCATTCATGCTTGAATCCTTCAGCAAAAGAAACCTCGAA 900
|||||
Db 841 TGTATGATCATATAGACGTGTCTCATTCATTCATGCTTGAATCCTTCAGCAAAAGAAACCTCGAA 900
QY 901 GCATATTTGAACCTGCAACCATATTTGAACCTCGACGAGAGAGCTTAAAGACACCGACAA 960
|||||
Db 901 GCATATTTGAACCTGCAACCATATTTGAACCTCGACGAGAGAGCTTAAAGACACCGACAA 960
QY 961 ATTAACCGCTTTCACACACAGTGGATCTTTAAACCGATCAAAACATAATTAATATAAT 1020
|||||
Db 961 ATTAACCGCTTTCACACACAGTGGATCTTTAAACCGATCAAAACATAATTAATATAAT 1020
QY 1021 ATATATACCTGTATACCTTATATATATATATAGTTTGTATTTGATTAATCTGTCT 1080
|||||
Db 1021 ATATATACCTGTATATACCTTATATATATATATAGTTTGTATTTGATTAATCTGTCT 1080
QY 1081 TGATCAAAAAAAGAAAAA 1104
|||||
Db 1081 TGATCAAAAAAAGAAAAA 1104

RESULT 3

US-09-277-716-31
: Sequence 31, Application US/09277715A
: Patent No. 6232107
: GENERAL INFORMATION:
: APPLICANT: Bryan, Bruce
: APPLICANT: Szent-Gyorgyi, Christopher
: APPLICANT: PROLINE, LTD.
: TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
: CURRENT APPLICATION NUMBER: US/09/277,716A
: CURRENT FILING DATE: 1999-03-25
: EARLIER APPLICATION NUMBER: 60/102,939
: EARLIER FILING DATE: 1998-10-01
: EARLIER APPLICATION NUMBER: 60/089,367
: EARLIER FILING DATE: 1998-05-15
: EARLIER APPLICATION NUMBER: 60/075,624
: EARLIER FILING DATE: 1998-03-27
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 31
: LENGTH: 1279
: TYPE: DNA
: ORGANISM: Ptiliosarcus gurneyi1
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (7)..(720)
: FEATURE:
: OTHER INFORMATION: Ptiliosarcus Green Fluorescent Protein (GFP) (Insert B)
US-09-277-716-31

Query Match 68.9% Score 760.2; DB 4: Length 1279;
Best Local Similarity 80.5%; Pred. No. 3.4e-193;
Matches 1026; Conservative 0; Mismatches 33; Indels 216; Gaps 3;

QY 28 GACAAATATACCGCAGCTATTTAAAGACACTGACGTGAAGAGATTAATGTGGCAAAA 87
|||||
Db 1 GACAAATATACCGCAGCTATTTAAAGACACTGACGTGAAGAGATTAATGTGGCAAAA 60
QY 88 GGTAGCGTTGAGAAATCGTGAACATCATGTTTTTCCATGCAAGAGATTTGGAAGAGC 147
|||||
Db 61 GGTAGCGTTGAGAAATCGTGAACATCATGTTTTTCCATGCAAGAGATTTGGAAGAGC 120
QY 148 AATGATATATTTGGAACCAATTCATGCAAAATCCGGGTTACAAAGGAGAGTCCGTTGCA 207

Db 121 AATGATATTTGGAACCAATTCATGCAAAATCCGGGTTACAAAGGAGAGTCCGTTGCA 180
|||||
QY 208 TTGCGTTTGCATATTTTTCATAGCTTTTCCAAATACGGGAATCGACTTTACGGAATAC 267
|||||
Db 181 TTGCGTTTGCATATTTTTCATAGCTTTTCCAAATACGGGAATCGACTTTACGGAATAC 240
QY 268 CCAGAGACATTCGGGAGTACTTTGTTCAATCATTCGCGGTGGATTTTCTTACGAAAGA 327
|||||
Db 241 CCAGAGACATTCGGGAGTACTTTGTTCAATCATTCGCGGTGGATTTTCTTACGAAAGA 300
QY 328 AATCTAGCTTTGAAATGCGCGCATTTGTGACATTCGTTAGATATTAAGTTAGAAAT 387
|||||
Db 301 AATCTAGCTTTGAAATGCGCGCATTTGTGACATTCGTTAGATATTAAGTTAGAAAT 360
QY 388 GATTAAGTTCACATACAAAGTGAATAGAGGCAACGGTTTCCATGTAACGAGACCGTG 447
|||||
Db 361 GATTAAGTTCACATACAAAGTGAATAGAGGCAACGGTTTCCATGTAACGAGACCGTG 420
QY 448 ATGCAAAAGCCATCTCGGCATGAGCCATCGTTTGAGGTGTCTAATGAACACCGGC 507
|||||
Db 421 ATGCAAAAGCCATCTCGGCATGAGCCATCGTTTGAGGTGTCTAATGAACACCGGC 480
QY 508 GTTCTGCTGGGCGAATAGATCTCGTTTACAAACCTGAGTCAAGGAAGTATTACTGTGC 567
|||||
Db 481 GTTCTGCTGGGCGAATAGATCTCGTTTACAAACCTGAGTCAAGGAAGTATTACTGTGC 540
QY 568 CACATGAAAACGTTTACAGATCCAAAGTGGAGTGAAGAATTCGCGAATATACCTTT 627
|||||
Db 541 CACATGAAAACGTTTACAGATCCAAAGTGGAGTGAAGAATTCGCGAATATACCTTT 600
QY 628 ATCCATCATGCTGTGAGAAACCTGCGTGAAGAAGAAAGTGTGGAACCAACGCGAG 687
|||||
Db 601 ATCCATCATGCTGTGAGAAACCTGCGTGAAGAAGAAAGTGTGGAACCAACGCGAG 660
QY 688 ACCGCCATTCGCAACACTGACCAATTTGAAAAACCTCTGGGCTCCCTTATGAAATGGGTG 747
|||||
Db 651 ACCGCCATTCGCAACACTGACCAATTTGAAAAACCTCTGGGCTCCCTTATGAAATGGGTG 720
QY 748 TGAATAATGCAATATACTGGGAAA----- 774
|||||
Db 721 TGAATAATGCAATATACTGGGAAAATTCACCAATATACTGGGAAAATGACCAATTTA 780
|||||
QY 775 ----- 774
Db 781 CTGGGGAATAATGCAATATACTGTAGAAAATTCACCAATATACTGGGGAATAATGACCAAT 840
|||||
QY 775 ----- 774
Db 841 TTACTGGGGAATGACCAATTTACTGTAGAAAATTCACCAATATACTGTGGAAAATGACCA 900
|||||
QY 775 -----CGATAACCGTTTGAAGCTT 795
|||||
Db 501 AATACTGTAGAAATGTTACACACTGGGTTGATTAACCGTTTGCATTAACCGTTTGAAGCTT 960
QY 796 GTGTATACAAATTTATTTGGGCGATTTTGTATGTGTATGTGTGTATGTATGATCAATTA 855
|||||
Db 961 GTGTATACAAATTTATTTGGGCGATTTTGTATGTGTATGTGTGTATGTATGATCAATTA 1020
QY 856 CGTCGATTCATTAAGTGTAAATCCTTCACGAAAAGAACTCGAAGCATATFAGAAACCTC 915
|||||
Db 1021 CGTCGATTCATTAAGTGTAAATCCTTCACGAAAAGAACTCGAAGCATATFAGAAACCTC 1062
QY 916 GAAGCATATTTGAACCTGAGGAGAGCGTAAAGAGACCGCAAAATTAACGCGTTTCAA 975
|||||
Db 1063 GAAGCATATTTGAACCTGAGGAGAGCGATAAAGAGACCGCAAAATTAATTAATA 1122
QY 976 CCAGCGATTGGAATCTTTAAACCGATCAAAACTATTAATATATATATATACCCGTGA 1034
|||||
Db 1123 CCAGCGATTGGAATCTTTAAACCGATCAAAACTATTAATATATATATATATACCCGTGA 1182
QY 1035 -----TAATCTATATATCTATATAGTTGATATTTGATTAATCTGTCTTATCAAAA 1089
|||||

Db 1183 CATATATATATATATATACATAGTTGATTTGATTTAAATCTGTTTGATCACTA 1242
QY 1090 AAAAAAAAAAAAAA 1104
Db 1243 AAAAAAAAAAAAAA 1257

RESULT 4
US-09-609-161B-31
; Sequence 31, Application US/09609161B
; Patent No. 6436682
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; APPLICANT: Szent-Gyorgyi, Christopher
; APPLICANT: PROLUME, LTD.
; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUC
; TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HI
; TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
; FILE REFERENCE: 24729-121B
; CURRENT APPLICATION NUMBER: US/09/609,161B
; PRIOR APPLICATION NUMBER: 09/277,716
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/102,939
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/089,367
; PRIOR FILING DATE: 1998-06-15
; PRIOR APPLICATION NUMBER: 60/079,624
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 31
; LENGTH: 1279
; TYPE: DNA
; ORGANISM: *Ptiliosarcus gurneyi*
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(720)
; OTHER INFORMATION: *Ptiliosarcus Green Fluorescent Protein (GFP) (Insert B)*
US-09-609-161B-31

Query Match 68.9%; Score 760.2; DB 4; Length 1279;
Best Local Similarity 80.5%; Pred. No. 3.4e-193;
Matches 1026; Conservative 0; Mismatches 33; Indels 216; Gaps 3;

QY 28 GACAATAATGAACCGGACGATTTAAAGAACACTGACGTAAGAGATATGTCGGCAAAA 87
Db 1 GACAAAATGACCGGACGATTTAAAGAACACTGACGTAAGAGATATGTCGGCAAAA 60
QY 88 GCTAGCGTTGAAGGAATCGTGAACAATCACTTTTTCATGGAAGATTTGAAAAAGC 147
Db 61 GCTAGCGTTGAAGGAATCGTGAACAATCACTTTTTCATGGAAGATTTGAAAAAGC 120
QY 148 AATGATATTTTGAAGAACCAATTTGATGCAATCCGGGTTACAAAGGAGGTCCTTGCCA 207
Db 121 AATGATATTTTGAAGAACCAATTTGATGCAATCCGGGTTACAAAGGAGGTCCTTGCCA 180
QY 208 TTGCGCTTCGATATGTTCCATAGCTTTCATACGGAATCGGACTTCGCAAGAAATAC 267
Db 181 TTGCGCTTCGATATGTTCCATAGCTTTCATACGGAATCGGACTTCGCAAGAAATAC 240
QY 268 CCAGACGACATTCGCGACTACTTTGTCATCATTCGCCGCTGATTTTTCACGANAAG 327
Db 241 CCAGACGACATTCGCGACTACTTTGTCATCATTCGCCGCTGATTTTTCACGANAAG 300
QY 328 AATTCAGCGTTTGAAGATGGCGCATTTGTCATTCGTTGCAATATAAGTTTAGAGAT 387
Db 301 AATTCAGCGTTTGAAGATGGCGCATTTGTCATTCGTTGCAATATAAGTTTAGAGAT 360
QY 388 GATAGGTTCCACTACAAAGTGGAGTATAGGCAACGGTTTCCCTAGTAGGAGACCCGGT 447
Db 361 GATAGGTTCCACTACAAAGTGGAGTATAGGCAACGGTTTCCCTAGTAGGAGACCCGGT 420

QY 448 ATGCAAAAAGCCATCCCTCGGACATGAGCCATCGTTTGAGGTGGTCTACATGAAACGCGC 507
Db 421 ATGCAAAAAGCCATCCCTCGGACATGAGCCATCGTTTGAGGTGGTCTACATGAAACGCGC 480
QY 508 GTTCTGTGGGCGAAGTATGATCTGTTTACAACTCGAGTCAAGGAACTATTACTCGTGC 567
Db 481 GTTCTGTGGGCGAAGTATGATCTGTTTACAACTCGAGTCAAGGAACTATTACTCGTGC 540
QY 568 CACATGAAAACGTTTACAGATCCAAAGCGAGTGAAGAAATTCGCCGAATATACCTTT 627
Db 541 CACATGAAAACGTTTACAGATCCAAAGCGAGTGAAGAAATTCGCCGAATATACCTTT 600
QY 628 ATCATCATCGTCTGGAGAAAACTACGTGGAAGAAGAGCTTGTTGTAACACACAGAG 687
Db 601 ATCATCATCGTCTGGAGAAAACTACGTGGAAGAAGAGCTTGTTGTAACACACAGAG 660
QY 688 ACGGCATTTGCACAACCTGACCAATTTGGAAAACTCTGGGCTCCTTCATGAAATGGGTG 747
Db 661 ACGGCATTTGCACAACCTGACCAATTTGGAAAACTCTGGGCTCCTTCATGAAATGGGTG 720
QY 748 TAGAAAATGACCAATATCTGGGAAA----- 774
Db 721 TAGAAAATGACCAATATCTGGGAAAATCCCAATATATCTGGGAAAATGACCAATTTA 780
QY 775 ----- 774
Db 781 CTGGGAAAATGACCAATATCTGTAGAAAATCACCATATATCTGGGAAAATGACCAAT 840
QY 775 ----- 774
Db 841 TTACTGGGAAAATGACCAATTTACTGTAGAAAATGACCAATATCTGTGAAAATGACCA 900
QY 775 -----CCGATAACCGTTTGAAGCTT 795
Db 901 AATATCTGACAAATCTTCACACTCGGTTGATACCCGTTTGATATACCGTTTGAAGCTT 960
QY 796 GTGATACAAATTTATTTGGGTCATTTTGTATGTGTATGTGTGTATGATCAATAGA 855
Db 961 GTGATACAAATTTATTTGGGTCATTTTGTATGTGTATGTGTGTATGATCAATAGA 1020
QY 856 CCGTCTCATCTTCACTTGAATCCCTTCACGCAAAAACAACTCGAAGCATTTGAACCTC 915
Db 1021 CCGTCTCATCTTCACTTGAATCCCTTCACGCAAAAACAACTCGAAGCATTTGAACCTC 1062
QY 916 GAAGCATATTTGAACCTCGAGCGAGAGCGTAAAGAGACCGCAATTTAACGCGTTTCAA 975
Db 1063 GAAGCATATTTGAACCTCGAGCGAGAGCATAAAGAGACCGCGACGATCAACAAATTTAATA 1122
QY 976 CCAGCAGTTGGAATCTTTAAACGATCAAACTATTTAATATAATATATATACCTGTA- 1034
Db 1123 CCAGCAGTTGGAATCTTTAAACGATCAAACTATTTAATATAATATATATACCTGTA- 1182
QY 1035 -----TACTTATATATATCTATAGTTTGAATTTGAATTTAAATCTGTTTGATCAAAA 1089
Db 1183 CATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1242
QY 1090 AAAAAAAAAAAAAA 1104
Db 1243 AAAAAAAAAAAAAA 1257

RESULT 5
US-09-609-161B-15
; Sequence 15, Application US/09609161B
; Patent No. 6436682
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; APPLICANT: Szent-Gyorgyi, Christopher
; APPLICANT: PROLUME, LTD.
; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
; TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS,
; FILE REFERENCE: 24729-121B

1 CURRENT APPLICATION NUMBER: US/09/609,161B
2 CURRENT FILING DATE: 2000-06-30
3 PRIOR APPLICATION NUMBER: 09/277,716
4 PRIOR FILING DATE: 1998-03-26
5 PRIOR APPLICATION NUMBER: 60/102,939
6 PRIOR FILING DATE: 1998-10-01
7 PRIOR APPLICATION NUMBER: 60/089,367
8 PRIOR FILING DATE: 1998-06-15
9 PRIOR APPLICATION NUMBER: 60/079,624
10 PRIOR FILING DATE: 1998-03-27
11 NUMBER OF SEQ ID NOS: 32
12 SOFTWARE: PatentIn Ver. 2.0
13 SEQ ID NO: 15
14 LENGTH: 1079
15 TYPE: DNA
16 ORGANISM: Renilla mulleri
17 FEATURE:
18 NAME/KEY: CDS
19 LOCATION: (259)..(975)
20 OTHER INFORMATION: Renilla mulleri Green Fluorescent Protein (GFP)
US-09-609-161B-15

Query Match 35.7%: Score 394.2; DB 4: Length 1079;
Best Local Similarity 71.4%: Pred. No. 8.5e-96;
Matches 519; Conservative 0; Mismatches 208; Indels 0; Gaps 0;

OY 27 AGACAAATGACCGGACGATTTAAAGACACGCTGACGAAAGAGATTATGCGCAAA 86
DB 253 AGATTAAGATGACTAAACAATATTTGAGACACTGCTTTACAAAGAGATGCTGATATA 311
OY 87 AGCTAGCGTTGAGGAATCGTGACAAATCGTTTTTTCATGGAAGCATTTGGAAAGC 146
DB 312 AGTAATCTCGAAGGAAATGTAAACACACCTGTTTACATGAGCGTTGGCGCAAGC 371
OY 147 CAATGATATTATTGGAACCAATTGCAAAATCGGGTTACAAAGCGAGTCCGTGCC 206
DB 372 GAATATTTTATTCGGCAATCAACTGTTCCGATTCCTGTCAGAAAGCGGCCCACTGCC 431
OY 207 ATTGCTTTGATTTGTTTCATAGCTTTGCAATGACGGAAATCCGACTTTCAGCAATA 266
DB 432 TTTTCATTTGATATTTGTTCTCACACGCTTTTCAATATGGAACCGGACTTTCAGCAATA 491
OY 267 CCCAGACGATTTGGGACACTTTGTTCAATCATTTCCCGCTGATTTTTCAGCAAG 326
DB 492 TCCGAAATGATATACAGATTATTTATACATCATTTCCAGCAGGATTTATGATGAAG 551
OY 327 AATCTACGCTTTGGAAGATGGCGCATTTGACATTCCTTACATATATGATTGAGACA 386
DB 552 AACATTACGTTAGGAAGATGGGCGACTGTTGAAATTCGTTGAGATATTAATAAGA 611
OY 387 TGATAGTTCCACTCAAGAGTGAGATAGAGGCAAGGCTTCCGACTAGACGCAACCGT 446
DB 612 AGACAAGTTTCGTTACAGAGTGGAATACAAAGGTAGTAACTTCCAGATGATGTCCTG 671
OY 447 GATGAAAAAGCCATCTCGGATGAGGCAATCGTTGAGTGTGCTACATGAACGACCG 506
DB 672 CATGCAAGACTATCTTAGAATAGAGCTTCATTTGAAGCCATGTAATGATGAATATG 731
OY 507 CTTTCTGGTGGCGGAAGATGATCTGCTTACAACTCGAGTGAAGCACTATTACTCGTG 566
DB 732 CGTCTGGTGGCGGAAGTATTTCTGCTATTAACCTAACTTGGGAAATATTTATTCATG 791
OY 567 GCACATGAAAGCGTTTACAGATTCGAAGCTGAGTGAAGAGATTTCCCGATATACACTT 626
DB 792 TCACATGAAAGCATTAATGAAGTCAAAAGGTGTAAGAGGATTTCTTCTGATATCATTT 851
OY 627 TATCCATCATCTGTTGGAAGAAACCTAGCTGGAAGGAAAGCTTCTGGAACAAACACA 686
DB 852 TATTCACATCTGTTGGAAGAAAGCTAGCTAGAGACGCGGCTTCGTTGACACACATGA 911
OY 687 GACGGCCATTCGACAAAGTACCAATTCGAATTCGAGTGGCTCCCTTCATGAATGGGT 746
DB 912 GACTGCTATTGCTCAATGATGATCTATAGGAAGAACCACTAGATGCTCTTACAGCAATGGGT 971

OY 747 GTAGAAA 753
DB 972 TTAACA 978

RESULT 6
US-09-277-716-15
1 Sequence 15, Application US/09277716A
2 Patent NO. 6232107
3 GENERAL INFORMATION:
4 APPLICANT: Bryan, Bruce
5 APPLICANT: Bryant-Gorydyl, Christopher
6 APPLICANT: PROLIME, LTD.
7 TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
8 CURRENT APPLICATION NUMBER: US/09/277,716A
9 CURRENT FILING DATE: 1999-03-26
10 EARLIER APPLICATION NUMBER: 60/102,939
11 EARLIER FILING DATE: 1998-10-01
12 EARLIER APPLICATION NUMBER: 60/089,367
13 EARLIER FILING DATE: 1998-06-15
14 EARLIER APPLICATION NUMBER: 60/079,624
15 EARLIER FILING DATE: 1998-03-27
16 NUMBER OF SEQ ID NOS: 32
17 SOFTWARE: PatentIn Ver. 2.0
18 SEQ ID NO: 15
19 LENGTH: 1079
20 TYPE: DNA
21 ORGANISM: Renilla mulleri
22 FEATURE:
23 NAME/KEY: CDS
24 LOCATION: (259)..(975)
25 OTHER INFORMATION: Renilla mulleri Green Fluorescent Protein (GFP)
US-09-277-716-15

Query Match 35.7%: Score 394.2; DB 4: Length 1085;
Best Local Similarity 71.4%: Pred. No. 8.5e-96;
Matches 519; Conservative 0; Mismatches 208; Indels 0; Gaps 0;

OY 27 AGACAAATGAAACCCGACGATTTAAAGACACGCTGACGAAAGAGATTATGCGCAAA 86
DB 252 AGATTAAGATGACTAAACAATATTTGAGACACTGTTTACAAAGAGATGCTGATATA 311
OY 87 AGCTAGCGTTGAGGAATCGTGACAAATCGGGTTACAAAGGAGTCCGTTGCC 146
DB 312 AGTAATCTCGAAGGAAATGTAAACACACCTGTTTACAAATGAGGCGTTGGCGCAAGC 371
OY 147 CAATGATATTATTGGAACCAATTGATGCAAAATCGGGTTACAAAGGAGTCCGTTGCC 206
DB 372 GAATATTTTATTCGGCAATCAACTGTTTTCAGATTTGTTGTACAGAAAGGCGCCACTGCC 431
OY 207 ATTGCTTTGATTTGTTTTCATAGCTTTTCAATAGCGGAATTCGCACTTTTCAGCAATA 266
DB 432 TTTTCATTTGATTTGTTGTTCTCACACGCTTTTCAATATGGAACCGGACTTTCAGCAATA 491
OY 267 CCCAGACGATTTGGGACACTTTGTTCAATCATTTCCCGCTGATTTTTCAGCAAG 326
DB 492 TCCGAAATGATATACAGATTATTTTATCAATCATTTCCAGCAGGATTTATGATGAAG 551
OY 327 AATCTACGCTTTGGAAGATGGCGCATTTGATGCAATTCGCTGAGATTAATGTTGGAAGA 386
DB 552 AACATTACGTTTACGAAGATGGGCGACTGTTTGAATTTCTTCTGATATTAATGATA 611
OY 387 TGATAGTTCCACTCAAGATGAGGATATAGAGCAACGCGTTTCCCTAGTAACGACCGCT 446
DB 612 AGACAAGTTTCGTTACAGAGTGGAATACAAAGGTAGTAACTTCCAGATGATGTCCTG 671
OY 447 GATGAAAAAGCCATCTCGGATGAGGCAATCGTTTGAAGTGTGCTACATGAAGAGCGG 506
DB 672 CATGCAAGACTATCTTAGAATAGAGCTTCATTTGAAGCCATGTATGAATGAATAATGG 731
OY 507 CTTTCTGGTGGCGGAAGTATGATCTGTTTACAACTGCAAGTGAAGGAACTATTACTCGTG 566

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Db 732 CGTCGTGTCGGCGAGAACTATTCCTGCTATAACTAACTGCGGAATATTATTCATG 791
Oy 567 CCACATGAAAAGCTTTTACATGCAAAAGGTGGAGTGAAGAATTCGCCGATATCACTT 626
Db 792 TCACATGAAACATTATATGAAGTGCAGAAAGGTGTAGTAAAGGCTTCTTCCTATCACTT 851
Oy 627 TATCATCATGCTGTGGAGAAACCTAGCTGAAGAGAAAGCTTCGTGAACAACACAGA 686
Db 852 TATTCACATGCTTTGGAAAAGACTTACGTAGAGACGGGGGCTTCGTTGAACACACATGA 911
Oy 667 GAGCGCCATTCACAACTGACCCACCAATTTGGAAAACCTCGGCTCCCTTCATGAATGGGT 746
Db 912 GACTGCTATTGCTCAATGACATCTATAGSAAACACTAGATCTTACAGCAATGGGT 971
Oy 747 GTAGAAA 753
Db 972 TTAACA 978
```

RESULT 7

```
US-09-459-956-7
: Sequence 7, Application US/09459956
: Patent No. 6342379
: GENERAL INFORMATION:
: APPLICANT: Gonzalez, III, Jesus E.
: TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
: FILE REFERENCE: REGEN1290-4
: CURRENT FILING DATE: 1999-12-13
: PRIOR FILING DATE: 1999-05-08
: PRIOR APPLICATION NUMBER: 08/481,977
: PRIOR FILING DATE: 1995-06-07
: PRIOR APPLICATION NUMBER: PCT/US96/09652
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 7
: LENGTH: 801
: TYPE: DNA
: ORGANISM: Clavularia sp
US-09-459-956-7
```

Query Match 14.5%; Score 160; DB 4; Length 801;
Best Local Similarity 56.9%; Pred. No. 1.7e-33;
Matches 314; Conservative 0; Mismatches 235; Indels 3; Gaps 1;

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Oy 95 TTGAAGGATCGTGAACATACGTTTTTTCATGAGAGATTTGGAAAAGCATGTAT 154
Db 167 TGGAAAGAAATGTAAACGGGCACTGCTTTTGTATCGAAGAGAAAGGAAAGCCCTT 226
Oy 155 TATTTGGAACCAATGTATGCAAAATCCGGGTTACAAAGGAGGTCCGTTGCCATTCGCTT 214
Db 227 ACGATGGGACACACACTTAAACCTGGAAGTGAAGAGGTGCGGCTCGCTTTTCTT 286
Oy 215 TCGATATTGTTCCATGACTTTCCATATCGGAATCGCACTTTCACGAATACCCAGACG 274
Db 287 ACGATATCTTGTCAAAACGGGTTCCAGTACGGAACAGACCATTTGCAAAATCCAGACG 346
Oy 275 ACATTTGCGACACTTGTGTCATTCGCCGGGTGAGATTTTTCACGAAAGCAAAATCTTAC 334
Db 347 ATATAGCCAGACTATTTCACAGCAGTCGTTCCGAGGAGATATTCCTGGGAAAGACCATGA 406
Oy 335 GCTTTGAAGTGGCCATTGTTGACATTCGTTAGATTTAGAAAGTGAATAGT 394
Db 407 CTTTGAAGACAAAGCATGTCAAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 466
Oy 395 TCCACTACAAAGTGAAGTGAAGGCAACGGTTTCCCTAGTGAAGGACCCGATGACAAA 454
Db 467 TTATCTATGAATTCGTTTGAAGGATGAACCTTCTCCCAATGCTCGGTTATGACAGA 526
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Oy 455 AAGCATCCTCGCATGAGGACCATCGTTTGAGTGTCTACATGAACAGCGGCTTGTG 514
Db 527 AAAAAGCTTTGAAGTGGAGAACCATCCACTGAGATTATBTAGTGCGTATGAGATGCGG 586
Oy 515 TGGCGAAGTAGATCTCGTTTACAACTGAGTCAAGGAACTATTACTGCTGCCACATGA 574
Db 587 TCGGAGATATTAGCATTTCTGTGCTGAGAGGAGGTGGCATTCGATGAGTGAATTCGA 646
Oy 575 AAAGCTTTTACAGATTCGAAGGTGGAGTGAAGAAATTCGCCGAATATCACTTTATTCATC 634
Db 647 AAAGATTATTACAAACGCAAAAAGTTGTCA---AATTGCCAGACTATCATCTTTGTGACC 703
Oy 635 ATCGTCTGAGA 646
Db 704 ATCGCATTTGAGA 715
```

RESULT 8

```
US-09-459-956-6
: Sequence 6, Application US/09459956
: Patent No. 6342379
: GENERAL INFORMATION:
: APPLICANT: Tsien, Roger Y.
: TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
: FILE REFERENCE: REGEN1290-4
: CURRENT FILING DATE: 1999-12-13
: PRIOR FILING DATE: 1999-05-08
: PRIOR APPLICATION NUMBER: 08/765,860
: PRIOR FILING DATE: 1995-06-07
: PRIOR APPLICATION NUMBER: 08/481,977
: PRIOR FILING DATE: 1996-06-06
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 6
: LENGTH: 678
: TYPE: DNA
: ORGANISM: Discosoma sp
US-09-459-956-6
```

Query Match 12.0%; Score 132.4; DB 4; Length 678;
Best Local Similarity 50.3%; Pred. No. 3.6e-26;
Matches 325; Conservative 0; Mismatches 321; Indels 0; Gaps 0;

```
Oy 55 AACACTGAGCTGMAAGAGATTATGTGGCAAAAGCTAGCTTGAAGAAATCGTGAACAAT 114
Db 13 AAGATGTATATCAAGACGTTTCATGAGTTTAAAGTTCCATGGAAGAAACGGTCAATGG 72
Oy 115 CACGTTTTTTCATGGAAGGATTTGGAAAAGCAATGTATTTTGGAAACCAATTTGATG 174
Db 73 CACGAGTTTGAATAGAAAGGCGAAGAGAGAGGAGGCCATACGAAGGCCACAAATCCGTA 132
Oy 175 CAATTCGGGTTACAAAGGAGGAGTCCGTTGCCATTCGCTTTCGATGATGTTTCCATTA 234
Db 133 AAGCTTAAGTAAACCAAGGGGAGACCTTTGGCATTTTGGGATATTTTGTGCACACAAA 192
Oy 235 TTCCAAATACGGGAATCGCACTTTCACGAATACCCAGAGACATTTGCGACACTATTGTT 294
Db 193 TTTGAGTATGGAAGCAGATATATGTCAAGCAACCTCGCGACATACCAAGACTATAAAG 252
Oy 295 CAATCATTTCCCGCTGAGATTTTTCACGAAGAAATCTACGCTTTTGAAGATGGCCCAT 354
Db 253 CTGTCAATTTCCGGAAGATTTTAAATGGGAAAGGTCATGAACCTTTGAAGACGCTGCG 312
Oy 355 GTTGACATTCGTTGAGATATAGTTTGAAGATGATTAAGTTCACATAAAGTGAAGTAT 414
Db 313 GTTACTGTAAACCCAGAGATTCAGTTTGCAGATGCTGTTTCATCTACAAAGGTCAAGTTC 372
Oy 415 AGAGCAACGGTTTCCCTAGTAAAGGACCCGATGACAAAAGGCAATCCTCGGCATGGAG 474
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Db 373 ATTGGCGTGAAGCTTCTTCCGATGAGACCTGTTATGCAAAAGAACATATGGCGTGGAA 432
OY 475 GCATCGTTTGAAGTGGCTACATGAAACAGCGGCTTCTGTCGGGCGAAGTACATTCGTT 534
Db 433 GCCAGCAGTACAGCTTTGATTCCTGCTGATGGCTGTAAAGGAAGATATCAAGGCT 492
OY 535 TACAACTGAGTCAAGGAACTATACCTGCGCCATGAAAGCGTTTATGAGATGCAAA 594
Db 493 CTGACAGTCAAGACCGGCTGCTACCTAGTTGAATTCAAAAGTATTTACATGGCAAG 552
OY 595 GGTGAGTGAAGAAATTCGCGGAATATCATTATCATCATGCTGTGAGAAACCTAC 654
Db 553 AAGCGTGTACAGTACCAAGGTAATGTTGATGCTCAAACTGATATACCAAGCCAC 612
OY 655 GTGGAAGAAAGAAAGCTTCTGTGGAACACAGAGAGCGCATTTGCAC 700
Db 613 AACGAAGACTATACAAATCGTTGAGCAGTATGAAGAACGAGGAGC 558
```

RESULT 9

```
US-09-459-956-5
: Sequence 5, Application US/09459956
: Patent No. 6342379
: GENERAL INFORMATION:
: APPLICANT: Tsien, Roger Y.
: APPLICANT: Gonzalez, III, Jesus E.
: TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
: FILE REFERENCE: RECENT190-4
: CURRENT APPLICATION NUMBER: US/09/459,956
: PRIOR FILING DATE: 1999-12-13
: PRIOR APPLICATION NUMBER: 08/765,860
: PRIOR FILING DATE: 1999-05-08
: PRIOR APPLICATION NUMBER: 08/481,977
: PRIOR FILING DATE: 1995-05-07
: PRIOR APPLICATION NUMBER: PCT/US96/09652
: PRIOR FILING DATE: 1995-05-06
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 5
: LENGTH: 699
: TYPE: DNA
: ORGANISM: Discosoma striata
US-09-459-956-5
```

```
Query Match 12.0%; Score 132.2; DB 4; Length 699;
Best Local Similarity 51.3%; Pred. No. 4.1e-26;
Matches 333; Conservative 0; Mismatches 313; Indels 3; Gaps 1;
```

```
OY 55 AACCTGCGACCTGGAAGAGATTATGTCGGCAAAAGCTAGCGTTGAGGAAATTCGTGAACAT 114
Db 13 AAGAGCTGATATGAAGAAAGAAATGTTGATGATCTTCATCTGGAAGCAAGCTTCAATGG 72
OY 115 CACGCTTTTCCATGGAAGATTTGGAAGGCAATGTATTTATTTGAACCAATGTATG 174
Db 73 CACTACTTTGAATATAAAGGCAAGGAAGAGCAAGCCATATGAAGGCAACATACCGTC 132
OY 175 CAAATCCGCTTACAAAGGAGGTCCTGTTCCATTCGCTTCGATATTTGTTCCATAGCT 234
Db 133 ACGCTCGAGTTACCAAGGAGTGGACCTTGCCATTGGTTGCTATATTTTGGCCACAA 192
OY 235 TTCCGATATCGGAGATCGGACTTTTCAGGAAATATCCGACAGCATTTGCGACTAGTTGT 294
Db 133 TTTCAAGTATGGAAGCAAGGCAATTTTCCACCCCTGACAAACATACATGATTTATCAAG 252
OY 295 CAATGATTCGCGCTGATTTTTCAGGAAGAAATCTACGCTTTGAAGATGGCCGATTT 354
Db 253 CTGTCATTTCCGAGGAGATATACATGCGAAGGTCATGCACTTTGAAGCGTGGCTTG 312
OY 355 GTTGACATTCCTTTCGATATATAGTTTACAGATGATAGTTCCTACACAACTGGAGTAT 414
Db 313 TGTGTATACCAATGATATGAGTTTGAACAGCAACGTGTTCTACTAGCATCAAGTTTC 372
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OY 415 AAGAGCAACGTTTCCCTAGTAAAGGACCCGATGAGCAAAAGCCATCTCGGCATGGAG 474
Db 373 ACTGGCTTAACTTCTCTCCAAATGAGCCGTTGTGCAAGAAAGCAACTGCGTGGGAA 432
OY 475 CCATCGTTTGAAGTGGCTACATGAAACAGCGGCTTCTGTCGGGCAAGTACATCTGTT 534
Db 433 CCGAGCAGTACAGCGTTTGTATCTCTGATGCTGTGTTTATAGAGACATTCATGCT 492
OY 535 TACAACTGAGTCAAGGAACTATACCTGCGCCATGAAAGCGTTTATGAGATGCAAA 594
Db 493 CTGACAGTGAAGAGAGGTGCTATACGCTGTGACATTTAAAGCTTTTACAGGGCCAG 552
OY 595 GGTGAGTGAAGAAATTCGCGGAATATCATTATCATCATGCTGTGAGAAA--ACC 651
Db 553 AAGCCCGCTTGAAGATGCGCAGGATATGTTGATGACCAACAACTGGTTATATGAGAC 612
OY 652 TACGTGGAAGAAAGAAAGCTTCTGTGGAACACAGAGAGCGCATTTGCAC 700
Db 613 AACGAAGAAATTCATGAAGATTTGAGGAGCATGGAATGCGCGTTCAC 661
```

RESULT 10

```
US-09-459-956-2
: Sequence 2, Application US/09459956
: Patent No. 6342379
: GENERAL INFORMATION:
: APPLICANT: Tsien, Roger Y.
: APPLICANT: Gonzalez, III, Jesus E.
: TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
: FILE REFERENCE: RECENT190-4
: CURRENT APPLICATION NUMBER: US/09/459,956
: PRIOR FILING DATE: 1999-12-13
: PRIOR APPLICATION NUMBER: 08/765,860
: PRIOR FILING DATE: 1999-05-08
: PRIOR APPLICATION NUMBER: 08/481,977
: PRIOR FILING DATE: 1995-06-07
: PRIOR APPLICATION NUMBER: PCT/US96/09652
: PRIOR FILING DATE: 1996-06-06
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 690
: TYPE: DNA
: ORGANISM: Anemonia majano
US-09-459-956-2
```

```
Query Match 10.1%; Score 111.2; DB 4; Length 690;
Best Local Similarity 50.4%; Pred. No. 1.6e-20;
Matches 272; Conservative 0; Mismatches 268; Indels 0; Gaps 0;
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OY 176 AATCCGCGTTACAAAGGAGGTCCTTGCATTCGCTTTTCATATTTGTTCCATAGCTT 235
Db 140 AAGTACACATGCGCAAGCTGGGCGCTTCGATTTCTCTTGACATACATCTACAGTGT 199
OY 236 TCCATATCGGCAATGCGACTTTTCACGAATATACCAAGAGACATTTGGGAGTACTTTGTC 295
Db 200 TCAAAATATGGAATGATGCTTTACTGCGTATCTACAGAGTATGCGCCGACTATTTCAAC 259
OY 296 AATCATTTCCGCGCTGATTTTCTACGAAGAAATCTACGCTTTGAAGATGGCGCATTTG 355
Db 260 AAGCATTTTCTTACGGAATGTATATGAAGAGACTTTTATACATATGAAGTGGAGAGTTG 319
OY 356 TTGACATTCGTTACAGATATAGTTTGAAGATAGTAACTTCCATCAAAAGTGGATATA 415
Db 320 CTACAGCCAGTTGGGAATATACCTTTAAAGGCAACTGCTTTGAGCACAAAATCCAGTTTC 379
OY 416 GAGGCAACGCTTTCCTTACGAAGCAAGCCGCTGATGCAAAAGCCATCTCTGCGCATGAGC 475
Db 380 ATGAGGTGAATTTCTCTGCTGATGAGCCTGTGATGCGAAGAGCAACATGATTTGGAGC 439
OY 476 CATCTTTGAGCTGTGTACATGAACAGGAGGCGTTCTGTGGCGCAAGTACATCTCGTTT 535
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Db 440 CATCTTTTGGAAAAATGACTGCTCTCCGATGGAATTTGAAGGGTATGTACACCGCGTTCC 499
Oy 536 ACAACCTGAGTCAGGAACTTATTACTGTCGCACATGAAAAAGTTTATACAGATCCAAAG 595
Db 500 TCATCTCTCAAGAGGATGGCAATTTACAGATGCCATTTCACACTCTTTTACAGACAAAAA 559
Oy 556 GTGAGTGAAGAAATTTCCCGAATATCACTTTATCCATCATCTGCTGAGAAAAACCTACG 655
Db 560 AACCGGTGACGATGCCACCAAAACCATGTGGTGACATGCGATTCGAGAGCCGACCTTG 619
Oy 656 TGGAGAAGAGAGCTTCTGTCGACACACAGAGCGCCATTGCAACAAGTACCAACATTTG 715
Db 620 ACAAAGGTGGCAACAGTGTTCAGCTGACGAGACGCTGTTCACATATAACCTCTGTTG 679

RESULT 11
US-09-459-956-3
: Sequence 3, Application US/09459956
: Patent No. 6342379
: GENERAL INFORMATION:
: APPLICANT: Tsien, Roger Y.
: APPLICANT: Gonzalez, III, Jesus E.
: TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
: FILE REFERENCE: REGEN1290-4
: CURRENT FILING DATE: 1999-12-13
: PRIOR FILING DATE: 1999-05-08
: PRIOR APPLICATION NUMBER: 08/765,860
: PRIOR FILING DATE: 1995-06-07
: PRIOR APPLICATION NUMBER: PCT/US96/09652
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 696
: TYPE: DNA
: ORGANISM: Zoanthus sp
US-09-459-956-3

Query Match 8.6%; Score 94.6; DB 4; Length 696;
Best Local Similarity 50.1%; Pred. No. 4.2e-16;
Matches 297; Conservative 0; Mismatches 284; Indels 12; Gaps 2;

Oy 61 GGACGTGAAGAGATTTATGCGCAAAAGCTAGCGTTGAAGAAATGCGTGAACAATCAGCTT 120
Db 19 GGTCTTAACAAAGAAATGCAATGAATACCGTATGGAAGGGTGGTGCATGACATTA 78
Oy 121 TTTTCCATGGAAGATTTGGAAGGCAATGTATTATTGGAACCAATTTGATGCAATC 180
Db 79 TTTTGATCAGCGGAGAGGCGATTTGGATATCCGTTCAAGGAAACAGCTATTATATCTG 138
Oy 181 CGGGTTACAAAGGAGTCCGTTGCCATTTCGTTCCGATTTGTTCCATTTGTTCCAA 240
Db 139 TGTGTGTCGAGGAGGAGCAATTTGCCGAAGACATTTGTCACCTGCTTAAAC 198
Oy 241 TACGGAATCGCACTTTTCAGAAATTCACGAGACATTTGCGGACTTTGTTGATCA 300
Db 199 TACGGAACAGGCTTTTCACTCAATATCTTCAAGACATGTTGACTATTTCAGAAACTCG 258
Oy 301 TTTCCGGCTGATTTTTCACGAAGCAATTCAGCTTTGAAGATGGCCCATTTGTTGAC 360
Db 259 TGTCCGCTGGATATACATGAGGAGCTTTTCTCTTTGAGAGTGGACAGTTTGCA 318
Oy 361 ATTTCGTTGATATAGTTTAGAGATGATAAGTTCCACTACAAAGTGGAGATATAGAGC 420
Db 319 TCTAATGCAATATAACAGTGTGTTGAAGAAACGTCATGATCATGATGATCAAAATTT 378
Oy 421 AACGG-----TTTCCCTAGTAAGGACCGGTGATGCAAAAAGCCATCTCGGCAATGGAG 474
Db 379 TATGGAGTAATTTTCTCTCTGATGGACCTGTGATGAAAAAAGATGACAGATTAACGTGGAG 438
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Oy 475 CCATCGTTTGAAGTGTCTA-----CATGAACAGCGCGCTTCTGTGGCGGAAGTATGAT 528
Db 439 CCATCTCCGAGGAAGATCATACCACTACCTTAAGCAGGGGATATTGAAGGGAGATGTCTCC 498
Oy 529 CTCGTTTCAAACTCGACTCAAGGCACTATTACTGTGTCGCACATGAAGCAAGCTTTACGA 588
Db 499 ATGTACCTCTCTTGTGAAGATGTGGCGCTTTACCGTCCCAATTCGACAGATTTACAAA 558
Oy 589 TCCAAAGGTGGAGTGAAGAAATTTCCGGAATATCACTTTATCCATCATCTCT 641
Db 559 GCAAGTGTGTGCCAAGAAAGATGCCGAGCTGGCACTTTCACACATTAAGCT 611

RESULT 12
US-09-459-956-4
: Sequence 4, Application US/09459956
: Patent No. 6342379
: GENERAL INFORMATION:
: APPLICANT: Tsien, Roger Y.
: APPLICANT: Gonzalez, III, Jesus E.
: TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
: FILE REFERENCE: REGEN1290-4
: CURRENT FILING DATE: 1999-12-13
: PRIOR FILING DATE: 1999-05-08
: PRIOR APPLICATION NUMBER: 08/765,860
: PRIOR FILING DATE: 1995-06-07
: PRIOR APPLICATION NUMBER: PCT/US96/09652
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 696
: TYPE: DNA
: ORGANISM: Zoanthus sp
US-09-459-956-4

Query Match 8.4%; Score 93; DB 4; Length 696;
Best Local Similarity 49.9%; Pred. No. 1.1e-15;
Matches 296; Conservative 0; Mismatches 285; Indels 12; Gaps 2;

Oy 61 GGACGTGAAGAGATTTATGCGCAAAAGCTAGCGTTGAAGAAATGCGTGAACAATCAGCTT 120
Db 19 GGTCTTAACAAAGAAATGCAATGAATATACCAATGGAAGGGTGGTGCATGACATTA 78
Oy 121 TTTTCCATGGAAGATTTGGAAGGCAATGTATTATTGGAACCAATTTGATGCAATC 180
Db 79 TTTTGATCAGCGGAGAGGCAATTTGGATATCCGTTCAAGGAAACAGACTATTATCTG 138
Oy 181 CGGGTTACAAAGGAGTCCGTTGCCATTTCGTTGATATTGTTCCATATCTTCCAA 240
Db 139 TGTGTGATCAGAGGAGGAGCAATTTGCCATTTCGGAAGACATATTGTCACTGTGTTAAG 198
Oy 241 TACGGAATCGCACTTTTCAGAAATTCACGAGACATTTGCGGACTTACTTTGTTCAATCA 300
Db 199 TACGGAACAGGATTTTCACTCAATATCTTCAAGACATGTAGACTATTTCAGAAACTCG 258
Oy 301 TTTCCGGCTGATTTTTCACGAAGCAATTCAGCTTTGGAAGATGGCGCCATTTGTTGAC 360
Db 259 TGTCCGCTGGATATACATGAGGAGGCTTTTCTCTTTGAGAGTGGACAGCTTGCA 318
Oy 361 ATTTCGTTGATATA-----AGTTAGAGATGATTAAGTTCCACTACAAAGTGGAGTAT 414
Db 319 TCCATGTAGATATAACAGTGTGCTCAAGAAACGTCATTTATCATTAAGACATATTT 378
Oy 415 AGAGCAACGCTTTTCCCTAGTAAGGACCGGTGATGCAAAAAGCCATCTCGGCAATGGAG 474
Db 379 AATGGAATGAATTTTCTCTCTGATGGACCTGTGATGAAAAAAGATGACAACTAATGGGAA 438
Oy 475 CCATCGTTTGAAGTGTCTACATG-----AACAGCGCGCTTCTGTGTGGCGCAAGTATGAT 528
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Db 439 GCATCCTGGAGAGATCATGCCAGTACCTAACGAGCGATACTGAAAGCGGATGCTCC 458
      ||| | ||| | ||| | ||| | ||| | ||| |
Qy 529 CTCGTTACAAATCCAGCAGCACTATTAATCTGTCGCCACATGAAAGCTTTACAGA 588
      ||| | ||| | ||| | ||| | ||| | ||| |
Db 459 ATGTACCTCTTCTTGAAGGATGTTGGCGCTTACCGGTGGCAGTTCGACACAGTTTACAAA 558
      ||| | ||| | ||| | ||| | ||| | ||| |
Qy 589 TCCAAAGTGGAGTGAAGATTCGCCGATATCACTTATCCATGATCTCT 641
      ||| | ||| | ||| | ||| | ||| | ||| |
Db 559 GCAACTGTCTGTCGCAAGTAAAGTCCGAGTGGCAGTCTGATGACGATTAAGCT 611

RESULT 13
5219739-8
: Patent No. 5219739
: APPLICANT: TISCHER, EDMUND G.; ABRAHAM, JUDITH A.; FIDDES,
: JOHN C.; MITCHELL, RICHARD L.
: TITLE OF INVENTION: DNA SEQUENCES ENCODING BVEGF120 AND
: HVEGF 121 AND METHODS FOR THE PRODUCTION OF BOVINE AND HUMAN
: VASCULAR ENDOTHELIAL CELL GROWTH FACTORS, BVEGF120 AND HVEGF121
: NUMBER OF SEQUENCES: 40
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/559,041
: FILING DATE: 27-JUL-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 450,883
: FILING DATE: 14-DEC-1989
: APPLICATION NUMBER: 387,545
: FILING DATE: 27-JUL-1989
: SEQ ID NO:8:
: LENGTH: 789

Query Match
Best Local Similarity 3.6%; Score 40.2; DB 6; Length 789;
Matches 68; Conservative 0; Mismatches 28; Indels 1; Gaps 1;

Qy 1009 ATTAAATTAATATATATACCTGTATA-ACCTATATATATCTATAGTTGATTTGA 1067
      ||| | ||| | ||| | ||| | ||| | ||| |
Db 683 ATTATATATATATATATATATATATATATAAATAATATATATATATATATATATATA 742
      ||| | ||| | ||| | ||| | ||| | ||| |
Qy 1068 TTAATCTGTTCTGTGATCAAAAAAAAAAAAAAAAA 1104
      ||| | ||| | ||| | ||| | ||| | ||| |
Db 743 TAAATAATATATATCTTTTAAAAAAAAAAAAAAAA 779

RESULT 14
US-07-867-106-2
: Sequence 2, Application US/07867106
: Patent No. 5389526
: GENERAL INFORMATION:
: APPLICANT: Slade, Martin R
: APPLICANT: Chaney, Andy G M
: APPLICANT: Williams, Keith L
: TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
: TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526.ris
: STREET: One Liberty Place 45th Floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/867,106
: FILING DATE: 19920623
: PRIOR APPLICATION DATA:
```

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: APPLICATION NUMBER: AU PJ 7187
: APPLICATION NUMBER: PCT/AU90/00530
: FILING DATE: 02-NOV-1989
: ATTORNEY/AGENT INFORMATION:
: NAME: Feeney, Joanne Longo
: REGISTRATION NUMBER: 35,134
: REFERENCE/DOCKET NUMBER: RICE-0002
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 215-568-3100
: TELEFAX: 215-568-3439
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5852 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: Single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 2378..5038
: NAME/KEY: CDS
: LOCATION: 2378..5038
: US-07-867-106-2

Query Match
Best Local Similarity 3.6%; Score 40; DB 1; Length 5852;
Matches 64; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 1001 TCAAACTATTATTAATATATATACCTGTATGATTAATATATATATATAGTTG 1060
      ||| | ||| | ||| | ||| | ||| | ||| |
Db 5369 TAAATTTAATATATATTAATTTTAAATTTGAAGTTCACAGATATATAGATTTAT 5428
      ||| | ||| | ||| | ||| | ||| | ||| |
Db 5429 TTAATTAATTTGAATTTTAAAAAAAAAAAAAAAA 5472

RESULT 15
5194596-8
: Patent No. 5194596
: APPLICANT: TISCHER, EDMUND G.; ABRAHAM, JUDITH A.; FIDDES, JOHN
: C.; MITCHELL, RICHARD L.
: TITLE OF INVENTION: PRODUCTION OF VASCULAR ENDOTHELIAL CELL
: GROWTH FACTOR
: NUMBER OF SEQUENCES: 32
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/450,883
: FILING DATE: 14-DEC-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 387,545
: FILING DATE: 27-JUL-1989
: SEQ ID NO:8:
: LENGTH: 790
: 5194596-8

Query Match
Best Local Similarity 3.6%; Score 39.4; DB 6; Length 790;
Matches 71; Conservative 0; Mismatches 31; Indels 3; Gaps 1;
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Qy 1003 AAACATTAATTAATATATATATATACCTGTAT-ACCTTATATATCTATATAGTTT 1059
      ||| | ||| | ||| | ||| | ||| | ||| |
Db 680 ACATTTATATATATATATATATATATATATTAATAAATAATATATATATTTATATA 739
      ||| | ||| | ||| | ||| | ||| | ||| |
Qy 1060 GATATTGATTAAATCTGTTCTGATCAAAAAAAAAAAAAAAAA 1104
      ||| | ||| | ||| | ||| | ||| | ||| |
Db 740 TATATAAAFATATATATCTTTTAAAAAAAAAAAAAAAA 784

Search completed: January 16, 2003, 11:04:29
Job time : 69.0554 secs
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Db	252	CGACAGCACTGCGCCGACCTACTTCGTGACAGAGCTTCCCTCCCGGCTTCTTCTACGACGGGA	311
Qy	330	TCCTACGCTTTGAAGATGGCGCCATTGTTCACATTCGTTTCAGATATTAAGTTTAAGAAGATGA	389
Db	312	CCTGGCGGTTTCAGAGGAGCGCGCCATCGTGACATCCGAGACGACATCAGCCTTGAGGAGCA	371
Qy	390	TAACTTCCACTACAAAGTGGAGTATAGAGCGCAAGGTTTCCCTAGTAACGGACCCGTGAT	449
Db	372	CAAGTTCACATACAAAGGTGAGTACCGCGGCAAGCGCTTCCCTACCAAGCGCCCTGTGAT	431
Qy	450	GCAAAAAGCCATCCCTCGGACATGAGGCCATTCGTTTGAAGGTGCTACTATGAACAGCGGCGT	509
Db	432	GCAGAGAGCCATCTCGGGGATGAGACCCAGCTTCGAGAGGTGGTGTACATGAAACAGCGGCGT	491
Qy	510	TCGTGTGGGCGAAGTAGATCTGCTTTACAAACTCGAGTTCAGGAACTATTAACGTGCGCA	569
Db	492	GCTGTGTGGGCGAGGTGAGCACTGTGTACACAGCTGGAACCGGCACTACTACAGTGCCA	551
Qy	570	CATGAAACGTTTTTCAGATCCAAAGGTGGAGTGGAAAGATATCCCGGAATATCACCTTAT	629
Db	552	CATGAAGACCTTCTTACCGGAGCAAGGCGGCGGTGAAGGATGTCCTGTGATACCTATTCAT	611
Qy	630	CCATATATGCTTGAGAAACCTACGTGGAAAGAAAGAACTTCGTGGAACAACAGCAGAC	689
Db	612	CCACACCGCGGCTGGAGAAAGAACTACGTGGAAGSAGGCGACCTTCGTGAGACACGACGAGAC	671
Qy	690	GGCCATTGCACAACTGACCCACAAATTGGAAAACTCTGGGCTCCCTTCATGAATTGGGTGA	749
Db	672	CGCCATTCGCCCGAGCTGAGCCACCATCGGCAAGCCTCTGGGCAAGCTGCACGAGTGGGTGA	731
Qy	750	GA 751	
Db	732	AA 733	

RESULT 2

US-09-795-040A-1

Sequence 1, Application US/09795040A

Patent No. US20020064842A1

GENERAL INFORMATION:

APPLICANT: Stratagene

TITLE OF INVENTION: Renilla Reniformis Green Fluorescent Protein and Mutants Thereof

FILE REFERENCE: 25436/1162

CURRENT APPLICATION NUMBER: US/09/795,040A

CURRENT FILING DATE: 2001-02-26

PRIOR APPLICATION NUMBER: US 60/185,589

PRIOR FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: 60/210,561

PRIOR FILING DATE: 2000-06-09

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1

LENGTH: 720

TYPE: DNA

ORGANISM: Renilla reniformis

FEATURE:

NAME/KEY: exon

LOCATION: (1)..(720)

OTHER INFORMATION: open reading frame

US-09-795-040A-1

Query Match	35.3%	Score 389.4;	DB 10;	Length 720;
Best Local Similarity	72.1%;	Pred. No. 5e-84;		
Matches 507;	Conservative 0;	Mismatches 196;	Indels 0;	Gaps 0

Oy	47	TATTAAGCAACACGCGACTGTAAGAAATATTATGTCGGCAAAAAGCTAGCGTTGGAGGAATCG	106
Db	17	TATTGGAACAAACACGCGAGTTGAGGAGACATCTGTTTAAAGTGATCTGGAAAGGTGAG	76
Oy	107	TGAACCAATCACGCTTTTTCATCGAAGAGATTGGAAAAAGCCAAATGTATTTATTTGGAACCC	166
Db	77	TAAACATCAATCATGTCTTCATCGAGAGGTTGTGGAAAAAGCAATATTTTATTTTCGGAAACC	136

Oy	167	AAAGATGCAAAATCCGGGTTTACAAAAGGAGAGCGTGGTCCATTCGGTTTGGATATATGTTT	225
Db	137	AACGTGGTTCACATTCGCTGTACCAAAAGGGGCCGGCTTCCATTTGGCATATTTCTCT	196
Oy	227	CCATAGCTTTCCAAATACGCGGATCGCACTTTCCAGAAATACCCAGACGACATTGCGGAGCT	286
Db	197	CACGAGCTTTCCATTAACGGCACACCGTACATTCACAGAAATACCCGGAGATATATCAGACT	256
Oy	287	ACTTTGTTCAAATCATCCCGGCTGGATTTTGTACGAAAGAAATCTACGCTTTGGAGATG	346
Db	257	TTTTTATACATTCATTTCCACGCGGATTTGTATACGAAGAACGTTGCCGTTACGAAGATG	316
Oy	347	GCGCCATGTTGACATTCGTTACATATTAAGTTAGAAAGATGATGAAGTTCACATACAAAG	406
Db	317	GTGCACTGGTTGAAATCCGTTCAATATTAATTTAAATTCGAGGAGATGTTGTCTACAGAG	376
Oy	407	TGGAGTATAGAGGCAACGGTTTCCCTAGTAACGGAACCCGGATGCAAAAAGCCATCCTCG	466
Db	377	TGGATATTAAGAGTATGTAATCTCCCGAATGATGTCAGATGATGAAGAACATATCAGAG	436
Oy	467	GCATGAGCCCATCGTTTGGAGTGTGTACATGAACAGCGGCGTTCTGGTGGGCGAAGTAG	526
Db	437	GATTACACACTTCGTTGGAATGTTGTATATGAACGATGCGCGTCTGGTTGGCCAAAGTCA	496
Oy	527	ATTCGTGTTTACAACCTCGAGTCAGGAGCACTTATCTGTCGCCACATGAAGAACTTTTACA	586
Db	497	TTCTGTGTTTATATGATTTAAACTCTGCGCAAAATTTTATTTGTCGTCCATGTAGAGAACTATGA	556
Oy	587	GATCCAAAGGTGGAGTGAAGCAATTTCCCGGAATATTCACATTATCATCATCGTCTGGAGA	646
Db	557	AATCAAGAGGTGATGTAGAGATTTTCCCGAATACCATTTTCATTCACATCGTTTAGAGA	616
Oy	647	AAACCTACGTGAAGAAAGAGCTTTCGTGAACAACACGAGAGCGCCATTGCCAACATGA	706
Db	617	AGACGTGATGTGAAGACGAGAGGTTTGTGTAGCAACACGAGAGCGCCATTGTCAACTGA	676
Oy	707	CCACATTTGGAAGAAACCTGTGGGCTCCCTTCATGTAATGGGTGA	749
Db	677	CATCGCTGGGGAACCACTTGATGTGATCTTACACGATGGGTTTTA	719

```

RESULT 3
US-10-060-857-5
; Sequence 5, Application US/10060857
; Patent No. US2002012318A1
; GENERAL INFORMATION:
; APPLICANT: Anticancer, Inc.
; APPLICANT: Zhao, Ming
; APPLICANT: Jiang, Ping
; APPLICANT: Xu, Mingxu
; APPLICANT: Yang, Meng
; TITLE OF INVENTION: IMPROVED FLUORESCENT PROTEINS
; FILE REFERENCE: 31276--20032.00
; CURRENT APPLICATION NUMBER: US/10/060.857
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: US 60/264,932
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Bifidobacterium longum
US-10-060-857-5

```

Query	Match	Similarity	33.1%	Score	365.6	DB	12	Length	720
Best Local	Similarity	70.1%	Pred.	No. 2.4e-78					
Matches	491	Conservative	0	Mismatches	209	Indels	0	Gaps	0
OY	50	TAAAGAACCTGCGACTGAAGAAGATTATTCGGCAAAACCTGCGCTTGAAGGAATCGTGA	109						
Db	20	TGAAGAACCCGCCCTCGCGAGATCATGTCTTTAAGGTGAACCTGCGAGGCAGTGCTGA	79						

```
QY 110 ACAATCAGCTTTTTCATGAGAGATTGGAAAGCAATGATTATTGGAAACCAAT 165
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 80 ACATCCAGCGTTTACCATGAGAGGCTGCGGCAAGGCAACATCTGTGGCAACACAG 139
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 170 TGTATGCAATCCGGGTTACAAAGGAGGTCGTTGCCATTTCGTTTCGATTTGTTCCA 229
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 140 TGGTGTAGATCCCGGTGACCAAGGGGCCCGTCCGTTCCGCTTCGACATCTCTCCC 199
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 230 TGGCTTTTCAATACGGAATCGCACTTTCAGCAATACGACAGACATTCGGGACTACT 289
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 200 CGGCTTCCAGTAGACGCAACCGCACTTACCAAGTACCGGAGGACATTCGCACTTCT 259
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 290 TTGTTCAATCATTTCCCGCTGGAATTTTCTACGAAAGAAATCGACCTTTGAAGATGCG 349
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 260 TCATCCAGTCTTCCCGCGCGGCTTGTAGSAGGCAACCGCTCCGCTACGAGACGCGG 319
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 350 CCATTGTTACATTTCTTACATATAGTTTAGAGATCATTAAGTTCCACTCAAAAGTGG 405
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 320 GCCTGTGAGATCCCGCTCCGACATCACTGATCGAGGAGATCTTGTTACCGGCTGG 379
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 410 AGTATGAGGCAACGGTTTCCCTACTAGCGAGCCGCGTANCAAAAAGCCATCTCGGCA 469
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 380 AGTACAGAGGCGCCCAACTTCCGACAGCGCGCGGTGATGAAGAACACATCACCGCC 439
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 470 TGGAGCCATCGTTTGAAGTGTCTACATGACAGCGCGCTTGTGGCGGAGTAGATC 529
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 440 TGCAGCGCTCTTGCAGGTGGTGTACATACAGACGCGCGTGTGGGCGAGGTATCC 499
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 530 TCGTTTACAACCTCGAGTACGGAACACTATTACTCGTGCACATGAACGTTTTCACAT 589
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 500 TCGTGTACCGCTGAACTCCGCAAGTCTACTCTCCGACATGCCACCTGATGAAGT 559
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 590 CCAAGCTGAGTGAAGAAATTCGCCGAATATCACTTTTCCATCTGCTGGAAGAAA 649
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 560 CCAAGGCGCTGTGAAGGACTTCCCGAGTACCACCTTCTCCAGACGCCCTGTGAAGAAA 619
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 650 CCTACGTGAGAGAGAACTTGTGGAACAACAGCAGCGCCATTGCAACAACGTGACCA 709
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 620 CCTAGTGAAGAGACGCGCTTGTGTGAGCAGAGACAGACCGCATGCCAGCTACCT 679
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 710 CAATTGGAACACTCTGGGCTCCCTTCATGATGGTGTA 749
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 680 CCCTGGGCAAGCGCTGGGCTCCCTCCAGAGAGTGCTGTA 719
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 4
US-10-060-857-3
: Sequence 3, Application US/10060857
: Patent No. US20020132318A1
: GENERAL INFORMATION:
: APPLICANT: Anticancer, Inc.
: APPLICANT: Zhao, Ming
: APPLICANT: Jjiang, Ping
: APPLICANT: Xu, Mingxu
: APPLICANT: Yang, Meng
: TITLE OF INVENTION: IMPROVED FLUORESCENT PROTEINS
: FILE REFERENCE: 31276-20032.00
: CURRENT APPLICATION NUMBER: US/10/060,857
: CURRENT FILING DATE: 2002-01-29
: PRIOR APPLICATION NUMBER: US 60/264,932
: PRIOR FILING DATE: 2001-01-29
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 720
: TYPE: DNA
: ORGANISM: Saccharomyces cerevisiae
US-10-060-857-3

Query Match 32.8%; Score 362.2; DB 12; Length 720;
Best Local Similarity 65.7%; Pred. No. 1,6e-77;
Matches 490; Conservative 0; Mismatches 213; Indels 0; Gaps 0;
```

```
QY 47 TATTAAAGAACACTGAGCTGAAAGAGATTATGCGCAAAAGCTAGCTTGAAGCAATCG 106
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 17 TTTTGAAGAAATATCGTGTTCGAAGAAATATTATGCTTTTAAAGTTAATTTGGAAGGTTTG 76
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 107 TGAACAATACGCTTTTTCATGAGAGATTTGGAAGAGCAATGATTATTTGGAACC 166
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 77 TTAATATCATGTTTATTATGAGAGGTTGGGTAAAGTAAATATTGTTGGTAATC 136
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 167 AATTGATGCAAAATCCGGGTTACAAAGGAGTCGTTGCCATTTCGTTTCGATATTGTTT 226
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 137 AATTGGTCAAAATTAAGATTAGTTAAAGGTCCATTTGGCAATTTGGATTGATTTTGT 196
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 227 CCATACCTTTCCAAATCGGGAATCGCACTTTCACGAAATACCGACAGCATTTGGGACT 286
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 197 CTCACGCTTTTCAATATGGAATATAGACTTTTACTAAATATCCAGAGATATTTCGATT 256
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 287 ACTTTGTTCAATCATTTCCCGCTGGAATTTTCTACGAAAGAAATCGACCTTTGAAGATG 346
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 257 TTTTATTCATCTTTTCCAGCTGTTTGTATTGAAAGAACTTGAATATGAAGATG 316
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 347 GCGCCATTGTTGACATTTGTTACATATAGTTTAGAAGATGATTAAGTTCCACTACAAG 406
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 317 GTGGTTTGGTTGAATTAAGATCTGATATTAATTTGATGAAGAAATCTTTGTTATAGAG 376
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 407 TCGAGTATGAGGCAACGGTTTCCCTAGTACGAGACCGGTGACAAAAGCCATCTCTCG 466
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 377 TTAATATTAAGGTAGAAATTTTCCAAATGATGCTCCAGATTTGAAAGAAACTATTACTG 436
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 467 GCATGAGGCAATCGTTTGAAGTGTCTACATGACAGCGCGCTTGTGGGCGAGTAG 526
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 437 GTTTCACACATCTTTTGAAGTTGTTATATGATGATGCTGTTTGGTTGGTCAAGTTA 496
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 527 ATCTGTTTACAACCTCGAGTACGGAACACTATTACTCGTCCACATGAAACGTTTACA 586
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 497 TTTTGGTTTATGATTGAATTTCTGTGAATTTATCTTGTATATGAAGAACTTTTGATGA 556
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 587 GATCCAAAGTGAAGTGAAGAAATTCGCCGAATATCACTTTATCCATCTGCTGAGACA 646
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 557 AATCTAAGGTGTGTTAAAGATTTTCCAGAAATATCATTTTATTCACATACATGGAAG 616
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 647 AAACCTACGTGAAGAGAACTTGTGGAACAACAGCAGCGCCATTGCAACAACCTGA 706
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 612 AAACCTATGTTGAAGATGCTGTTTGTGGAACAACATGAACACTGCTATTTGCTCAATTGA 676
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 707 CCACAATTGGAACACTCTGGGCTCCCTTCATGATGGTGTA 749
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 677 CTTCTTTTGGTAAACCATTTGGGTTCTTTCATGATGGGTTTA 719
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 5
US-10-060-857-4
: Sequence 4, Application US/10060857
: Patent No. US20020132318A1
: GENERAL INFORMATION:
: APPLICANT: Anticancer, Inc.
: APPLICANT: Zhao, Ming
: APPLICANT: Jjiang, Ping
: APPLICANT: Xu, Mingxu
: APPLICANT: Yang, Meng
: TITLE OF INVENTION: IMPROVED FLUORESCENT PROTEINS
: FILE REFERENCE: 31276-20032.00
: CURRENT APPLICATION NUMBER: US/10/060,857
: CURRENT FILING DATE: 2002-01-29
: PRIOR APPLICATION NUMBER: US 60/264,932
: PRIOR FILING DATE: 2001-01-29
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 720
: TYPE: DNA
: ORGANISM: Escherichia coli
US-10-060-857-4
```



```

: CURRENT FILING DATE: 2002-01-29
: PRIOR APPLICATION NUMBER: US 60/264,932
: PRIOR FILING DATE: 2001-01-25
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: FASTED for Windows Version 4.0
: SEQ ID NO: 2
: LENGTH: 720
: TYPE: DNA
: ORGANISM: Renilla reniformis
US-10-060-857-2
```

```

Query Match      30.1% Score 332.6; DB 12; Length 720;
Best Local Similarity 66.6%; Pred. No. 1.9e-70;
Matches 476; Conservative 0; Mismatches 239; Indels 0; Gaps 0;
```

```

QY 35 TGAACCGCAGCTATTAAAGAACACTGCACTGAAGAGATTATGTCGCAAAAGCTAGCG 94
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 5 TGACGACGAGATCCCTGGAAGAACACCGCGCTCGAGAGATCATGACCTTCAGAGTGAACC 64

QY 95 TTGAAGGAATCGTGAACATCACTGTTTTCATGGAAGCATTTTGGAAAAGCAGATGTAT 154
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 65 TGAGAGCGCTGGTGAACAAACCACTGTTTACCATGAGAGGCTCGGCAAGGCAACATCC 124

QY 155 TATTTGGAACCAATGTATGCAAAATCCGGGTTACAAAGGAGAGTCCGTTGCCATTGCTT 214
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 125 TGTTCGGCAACACAGCTGTGTGAGATCCGCGTGACCAAGGGCGGCCCCCTTGCCCTTGCT 184

QY 215 TCGATATTGTTTCATAGCTTTCCCAATACGGGATTCGACACTTTCAGCAAAATACCCAGAG 274
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 185 TCGATATCTTGAGCCCGCGCTTCAGTACGGACACCGCTTACCAAGTACCCCGAGG 244

QY 275 ACATTGGCGACTACTTGTTCATCATCTCCCGGCTGGATTTTTCATGGAAGCAAAATCTAC 334
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 245 ACATCAGCAGCTTTTCATCTCAGAGCTTCCCGCGGCTTCGTGAGAGCGCACCTTCG 304

QY 335 GCTTTGAAGATGGCCCATTTGTGACATTCGTTCAAGATTAAGTTAGAATGATAGT 394
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 305 GCTAGCAGAGACGGCGGCTGTGTGAGATCCGACGACATCAACCTGATCGAGAGATGT 364

QY 395 TCCACTACCAAGTGAATATAGAGGCAAGCGTTTCCCTAGTAACGGACCCGATGATGCAAA 454
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 365 TCGTGTACCGCTGTGAGTACGAAGGGCGGCACTTCCCCAACGACGGCCCCGTCATGAMA 424

QY 455 AAGCCATCTCGGCATGAGAGCCATCGTTGAGGTGTCATGTAACAGACGGGCTCTGG 514
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 425 AGACCATCAACCGGCTCGACGCCAGCTTCGAGGTGTGTACATGAACGAGCGGTCTGG 484

QY 515 TGGCGGAAGTAGATCTCGTTTACAAACTGAGTCAAGGAACATATTACTGTCACATGCA 574
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 485 TGGGCCAGGTGATCTGTGTACCGCTGACCGCTGACAGCGGCAAGTTTACACCTGCCACATGC 544

QY 575 AAACGTTTACAGATCGAAGGTGAGTAAAGAAATTCGCCGAATATCATCTTTATTCATC 634
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 545 GCACCTGTATGAGAGCAAGGGCTGTGTGAAGACTTCCCCAGATACCACTTATTCACAGC 604

QY 635 ATCGTCTGAGAAACGTAAGTGAAGAGAAAGCTTCCTGGAACAAACGAGAGCGCA 694
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 605 ACCGCTGTGAGAGAACCTATGCTGAGAGAGCGCGCTTCCTGAGACAGCAACGACCGCCA 664

QY 695 TTGACAACTGACCAATTTGAAAAACCTCTGGGCTCCCTTGATGAATGGGTGTA 749
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 665 TCGCCAGCTGACAGCGCTGGGCAAGCCCTGGGCAAGCTGTGACAGAGTGGGTGTA 715
```

```

RESULT 8
US-09-967-772-7
: Sequence 7, Application US/09967772
: Patent No. US20020164577A1
: GENERAL INFORMATION:
: APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
: APPLICANT: TSIBEN, Roger
: APPLICANT: GONALEZ, Jesus
: TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY OPTICAL METHODS
```

```

: FILE REFERENCE: REGN1290-5
: CURRENT APPLICATION NUMBER: US/09/967,772
: CURRENT FILING DATE: 2001-09-28
: PRIOR APPLICATION NUMBER: US 09/459,956
: PRIOR FILING DATE: 1999-12-13
: PRIOR APPLICATION NUMBER: US 08/765,860
: PRIOR FILING DATE: 1996-12-19
: PRIOR APPLICATION NUMBER: PCT/US96/09652
: PRIOR FILING DATE: 1996-06-06
: PRIOR APPLICATION NUMBER: US 08/481,977
: PRIOR FILING DATE: 1995-06-07
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 7
: LENGTH: 801
: TYPE: DNA
: ORGANISM: Clavularia sp
US-09-967-772-7
```

```

Query Match      14.5% Score 160; DB 9; Length 801;
Best Local Similarity 56.9%; Pred. No. 3.5e-29;
Matches 314; Conservative 0; Mismatches 235; Indels 3; Gaps 1;
```

```

QY 95 TTGAAGGAATCGTGAACATCACTGTTTTCATGGAAGGATTTGGAAGCAATGTAT 154
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 167 TGAAGCAAAATGTAAGGCGGCTGCTTTGTGATCGAAGAGAGAGAAAGCAAGCTT 226

QY 155 TATTTGGAACCAATGTATGCAAAATCCGGGTTACAAAGGAGAGTCCGTTGCCATTGCTT 214
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 227 ACGATGGGACACACACTTAAACCTGAGAGTGAAGAGAGTGGCGCTTGCCCTTTTCTT 286

QY 215 TCGATATTGTTTCATAGCTTTCCCAATACGGGATTCGACACTTTCACGAAATACCCAGAG 274
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 287 ACGATATCTTGTCAAACGGGTTCCAGTACGGAACAGACACTTGGACAAATACCCAGAG 346

QY 275 ACATTGGCGACTACTTGTTCATCATCTCCCGGCTGGATTTTTCGAAAGAAATCTAC 334
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 347 ATATAGCAGACTATTTCAGCAGCTGCTTCCGAGGATATTCTGGGAAGAACCATGA 406

QY 335 GCTTTGAAGATGGCGCATTTGTGACATTCGTTCAAGATTAAGTTAGAATGATAGT 394
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 407 CTTTGGAGAACAAAGGCACTTGTCAAGTGAAGAAAGTACATTAAGCATGAGGAAGACTGCT 466

QY 395 TCCACTACCAAGTGAAGTATAGAGCAAGGTTTCCCTAGTAACGGACCCGATGATGCAAA 454
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 467 TTATCTATGAATTCGTTTGTGATGGATGAACCTTCTCCATGCTCGGTTATGACAGA 526

QY 455 AAGCCATCTCGGCATGAGAGCCATCGTTGAGGTGTCATGTAACAGACGGGCTCTGG 514
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 527 AAAAAAATTGAAAGGAGAACCATCCACTGAGATTAATGTACGTGCCTGATGAGAGTCTGG 586

QY 515 TGGCGGAAGTAGATCTCGTTTACAAACTGAGTCAAGGAACATATTACTGTCGCCACATGA 574
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 587 TCGAGATATTTAGCCATCTCTGTTGCTGAGAGGAGTGGCATTACCATGATGACTTCA 646

QY 575 AAACGTTTACAGATCCAAAGGTGAGTAAAGAAATTCGCCGAATATCATCTTTATTCATC 634
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 647 AAAGTATTTACAAAGCAAAAAAAGTTGTCA--AATTGCCAGACTATCACTTTGTGAGCC 703

QY 635 ATCGTCTGAGAGA 646
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 704 ATCGCATTGAGA 715
```

```

RESULT 9
US-10-006-922-3
: Sequence 3, Application US/10006922
: Publication No. US20020197676A1
: GENERAL INFORMATION:
: APPLICANT: Lukyanov, Sergey A
: APPLICANT: Fradkov, Arcady F.
: APPLICANT: Labas, Yulii A.
: APPLICANT: Matz, Mikhail V.
```

```
APPLICANT: Tersikh, Alexey
TITLE OF INVENTION: No. US20020197676a1el Chromophores/Fluorophores and
FILE REFERENCE: CLON-035CIP
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/120,330
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: 09/457,898
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/458,144
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/458,477
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/457,556
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/444,338
PRIOR FILING DATE: 1999-11-19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 3
LENGTH: 1116
TYPE: DNA
ORGANISM: Clavularia species
FEATURE:
NAME/KEY: misc.feature
LOCATION: 8, 12, 13, 17, 65, 77, 102, 104
OTHER INFORMATION: n = A,T,C or G
US-10-006-922-3
```

```
Query Match          14.5%; Score 160; DB 9; Length 1116;
Best Local Similarity 56.9%; Pred. No. 4e-29;
Matches 314: Conservative 0; Mismatches 235; Indels 3; Gaps 1;
```

```
QY 95 TTGAAGGAATCGTGAACATCACTTTTCCATGAGAGATTGGAAAAGCCATGTAT 154
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 317 TCGAAGGAATGTAAACGGCATGCTTTGTGATCGAAGAGAGAGAGAGCCCTT 376
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 155 TATTTGGAACCAATGTATGATCGGATTCACAAAGGAGAGTCCGTTGCCATTCG 214
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 377 ACGATGGGACACACACTTTAAACCTGGAGTGAAGAGAGTGCCTCTGCTTTTCTT 436
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 215 TCGAATATGTTTCATAGCTTTCATACGAGGATCGACTTTTCAGAAATCCAGAC 274
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 437 ACGATATCTTGTCAACGCGGTTCCAGTACGAAACAGACATTTACAAATACCCGAC 496
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 275 ACATTCGCGACACTTGTTCATCATCTCCCGGCTGGATTTTCTTACGAAAGAACTAC 334
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 497 ATATAGCAGACTATTTCAAGCAGTCCGTTCCGAGGATATTCCTGGAAAGAACCATGA 556
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 335 GCTTGAAGATGGCGCATTTGTACATTCGTTACATATAGTTAGAGATGTATAGT 394
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 557 CTTTGAAGACAAAGCATTTGTCAAAAGTGAAGTACATTAAGCATGAGAGAGATCCT 616
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 395 TCCACTACAAGTGAAGTATAGAGCAGGTTTCCCTAGTAACGAGACCCGTGATGCAA 454
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 617 TATATGAAATTCGTTTGTGATGGATGAATTCCTCCCAATGGTCCGTTATACAGA 676
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 455 AAGCCATCTCGGATGAGAGCATCTTTGAGTGTCTACATGAAGACGGCGCTTCTGG 514
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 677 AAAAACTTTGAAGTGGAGAACCATCCAGATTAATGATGCGCTGATGGAGTCTGG 736
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 515 TGGGCAAGTATGATCGTTTACAAACCTGAGTCAAGAGAACTATTACCTGTCACATGA 574
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 737 TCGGAGATATTAGCCATTCTCTGTCTGAGAGAGAGTGGCCATTACCATGTGACTTGA 796
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 575 AAACGTTTACAGATCCAAAGGTGAGTGAAGAAATTTCCCGGAATATCACTTTATCATC 634
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 797 AAAGTATTTACAAAGCAAAAAAGTTGTCA---AATTGCCAGACATATCACTTTGTGAGAC 853
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 635 ATCGTCTGGAGA 646
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 854 ATCGCATTTGAGA 865
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
RESULT 10
US-10-006-922-9
Sequence 9, Application US/10006922
Publication No. US20020197676a1
GENERAL INFORMATION:
APPLICANT: Lukyanov, Sergey A.
APPLICANT: Fradkov, Arcady F.
APPLICANT: Labas, Yulii A.
APPLICANT: Matcz, Mikhail V.
APPLICANT: Tersikh, Alexey
TITLE OF INVENTION: No. US20020197676a1el Chromophores/Fluorophores and
FILE REFERENCE: CLON-035CIP
CURRENT APPLICATION NUMBER: US/10/006,922
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/120,330
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: 09/457,898
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/458,144
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/458,477
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/457,556
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/444,338
PRIOR FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 9
LENGTH: 850
TYPE: DNA
ORGANISM: Disosoma striata
US-10-006-922-9
```

```
Query Match          12.6%; Score 138.8; DB 9; Length 850;
Best Local Similarity 50.9%; Pred. No. 4.2e-24;
Matches 329: Conservative 0; Mismatches 317; Indels 0; Gaps 0;
```

```
QY 55 AACCTGAGCTGAAGAAGATTAATGTCGCAAAAAGCTAGCGTTGAAGAAATCGTGAACAT 114
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 54 AAGAGTGTGATCAACGAAGAAATTTGATCATCTTCACTGGAAGAAAGCTTCAATGCG 113
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 115 CACGTTTTTCCATGGAAGGATTTGGAAGAGCAATGTATTATTGGAACCAATGTATG 174
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 114 CACTACTTTGAATATAAAGGCAAAAGGAAAGGAGCCCTAATGAAGGACCAATACGCTC 173
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 175 CAATTCGCGGTACAAAGGAGGTCGTTGCCATTCGCTTTCGATATTTGTTCCATAGCT 234
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 174 ACGCTCGAGGTACCAAGAGGTGACCTCTCCCATTTGGTGGCATATATTTGGCCACAA 233
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 235 TTCCAAATACGGAATCGCACTTTACAGAAATACCAAGACGACATTTGCGACTACTTTGTT 294
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 234 TTTCAGTATGGAAGAAAGCAATTTCTCCACCACCTCGACATACCTGATTAATCTAAG 293
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 295 CAATCATTCGCGGTGAGATTTTTCACGAAGAAATTCAGCTTTGGAAGATGGCGCCATT 354
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 294 CTGTCAATTCGCGAGGATATACATGAGACGCTCATGCACTTTGGAAGACGGTGGCTTG 353
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 355 GTTGCAATTCGTTCAAGATTAAGTTTGAAGATGATTAAGTTTCCATACAAAGTGGATAT 414
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 354 TGTGTATACCAATGATATGATGTTGACAGGCAACTGTTTCACTAGACATCAAGTTTC 413
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 415 AAGGCAACGTTTCCCTAGTAACGAGACCCGTGATGCAAAAAAGCCATCCTCGGCATGAG 474
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 414 ACTGCGTTGAACCTTTCCTCAATGAGACCCGTTGTGCAAGAAAGCAACTGCTGGCAA 473
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 475 CCATCGTTTGAAGTGTCTACATGAACAGCGGCTTTCGTCGTGGGCAAGTACATCTCGTT 534
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 474 CCGAGCACTGAGCGTTTGTATCTCTCGTATGAGCGGTTGATGAGAGACATCATCATCTCT 533
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
OY 535 TACAACTCGAGTCAGGAGACTATTACTGTCGCCACATGAAAGCTTTTACACATCCAA 594
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 534 CTCACAGTGAAGAGAGCGTGCATTCATGATGATGACATTAAACGCTTTTACAGGGCCAA 593
OY 595 GGTGGAGTGAAGAATATCCCGGAATATCATTATCATCATCTGTCGGAGAAACCTTAC 654
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 594 AAGCCCGTAAAGATGCCAGGATATGATGTTTGACACCAACTGCTTAATAGAGCAAC 653
OY 655 GTGGAGAAGAGAGCTTCGTGGACACAGAGAGCGGCATTGCAC 700
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 654 GACAAAGAAATTGATGAAAGTTGAGAGCATGAAATCCCGCTTGAC 699
```

RESULT 11

```
US-09-967-772-6
: Sequence 6, Application US/09567772
: Patent No. US20020164577A1
: GENERAL INFORMATION:
: APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
: APPLICANT: TSJEN, Roger
: APPLICANT: GONZALEZ, Jesus
: TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY OPTICAL METHODS
: FILE REFERENCE: REGEN1290-5
: CURRENT APPLICATION NUMBER: US/09/967,772
: PRIOR FILING DATE: 2001-09-28
: PRIOR APPLICATION NUMBER: US 09/459,956
: PRIOR FILING DATE: 1999-12-13
: PRIOR APPLICATION NUMBER: US 08/765,860
: PRIOR FILING DATE: 1996-12-19
: PRIOR APPLICATION NUMBER: PCT/US96/09652
: PRIOR FILING DATE: 1996-06-06
: PRIOR APPLICATION NUMBER: US 08/481,577
: PRIOR FILING DATE: 1995-06-07
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 6
: LENGTH: 678
: TYPE: DNA
: ORGANISM: Discosoma sp "red"
US-09-967-772-6
```

```
Query Match 12.0%: Score 132.4; DB 9; Length 678;
Best Local Similarity 50.3%: Pred. No. 1.3e-22;
Matches 325; Conservative 0; Mismatches 321; Indels 0; Gaps 0;
```

```
OY 55 AACACTGACGTGAAGAGATTATGTGCGCAAAAGCTAGCGTTGAAGAAATCGTGAACAAT 114
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 13 AAGAATGTTATACAGAGAGTTCAGAGCTTTAAGGTTCCCATGGAAGAAACGGTCAATGG 72
OY 115 CACGTTTTTTCATGGAAGCATTTTGGAAAAGCAATGTAATTTTGGAAACCAATTGATG 174
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 73 CACGAGTTTGAATATGAAGAGCGAAGAGAGGAGGCCATACGAAGGCCAATACCGTA 132
OY 175 CAATTCGGGTTACAAAGGAGTCCGTTGCCATTCGTTTCGATATTTGTTCCATAGCT 234
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 133 AAGCTTAAGTAAACCAAGGGGAGCTTTGCCATTTGCTTGGGATATTTTGTACACAAA 192
OY 235 TTCGAATACGGAATTCGCACTTTCACGAATATCCAGACGACATTCGGGACTACTTTGTT 294
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 193 TTTGACTATGGAAGCAAGCTATATGTCAAGCACCTGCCGACATACCACTATATAAAG 252
OY 295 CAATCATTCGCGGCTGATTTTCTTACGAAGAATCTATGCGTTTGAAGATGCGGCGCAT 354
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 253 CTGTATTTCTGAAGAGATTTAAATGGGAAGGGTCATCACTTTGAAGACGGTGGCTG 312
OY 335 GTTGACATTCGTTGATATTAAGTTTGAAGATGATAACTTCACATCAAAAGTGAAGTAT 414
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 313 GTTACTGTAAACCAAGATTCAGTTTCAGAGATGGCTGTTTCATCTACAAAGTCAAGTTC 372
OY 415 AGAGCAACGGTTTCCCTAGTAAAGGAGCGGTGATGACAAAAGCCATCTCCGCGATGAG 474
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 373 ATTGGCTGAACTTCCTCCGATGGACCTGTTATGCAAAAGACGAATGGGCTGGGAA 432
```

```
OY 475 CCATCGTTTGAGGTGCTACATGAACACCGCGCTTCTGTGGCGCAACTAGATCTCGTT 534
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 433 GCCAGACATGAGCGTTTGTATCTCTGATGATGGCGTTGTAAAGAGACGATTCATAGCGT 492
OY 535 TACAACTCGAGTCAGGAGACTATTACTGTCGCCACATGAAAGCGTTTACAGATCCAA 594
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 493 CTGAACCTGAAGAGCGGTGCTCATCTAGTTGAAATTCAAAAGTATTTATCATGCGCAAG 552
OY 595 GGTGGAGTGAAGAATATCCCGGAATATCATTATTCATCATCTGTCGGAGAAACCTAC 654
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 553 AAGCTGTGCAGTACCAAGGATGACTATATGTTGACTCCAACTGGATTAACAAAGCCAC 612
OY 655 GTGGAGAAGAGAGCTTCGTGGACACACAGAGAGCGGCATTGCAC 700
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 613 AACGAAGACTATATGATCTGTTGAGCAGTATGAAGAACCGAGGAGAC 658
```

RESULT 12

```
US-10-006-922-11
: Sequence 11, Application US/10006922
: Publication No. US20020197676A1
: GENERAL INFORMATION:
: APPLICANT: Lukyanov, Sergey A
: APPLICANT: Fradkov, Arcady F.
: APPLICANT: Labas, Yulij A.
: APPLICANT: Matz, Mikhail V.
: TITLE OF INVENTION: No. US20020197676A1el Chromophores/Fluorophores and
: FILE REFERENCE: Methods for using the Same
: CURRENT APPLICATION NUMBER: US/10/006,922
: PRIOR FILING DATE: 2001-12-04
: PRIOR APPLICATION NUMBER: 09/120,330
: PRIOR FILING DATE: 1998-12-11
: PRIOR APPLICATION NUMBER: 09/457,898
: PRIOR FILING DATE: 1999-12-09
: PRIOR APPLICATION NUMBER: 09/458,144
: PRIOR FILING DATE: 1999-12-09
: PRIOR APPLICATION NUMBER: 09/458,477
: PRIOR FILING DATE: 1999-12-09
: PRIOR APPLICATION NUMBER: 09/457,556
: PRIOR FILING DATE: 1999-12-09
: PRIOR APPLICATION NUMBER: 09/444,338
: PRIOR FILING DATE: 1999-11-19
: NUMBER OF SEQ ID NOS: 46
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 11
: LENGTH: 678
: TYPE: DNA
: ORGANISM: Discosoma species
US-10-006-922-11
```

```
Query Match 12.0%: Score 132.4; DB 9; Length 678;
Best Local Similarity 50.3%: Pred. No. 1.3e-22;
Matches 325; Conservative 0; Mismatches 321; Indels 0; Gaps 0;
```

```
OY 55 AACACTGACGTGAAGAGATTATGTGCGCAAAAGCTAGCGTTGAAGAAATCGTGAACAAT 114
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 13 AAGAATGTTATACAGAGAGTTCAGAGCTTTAAGGTTCCCATGGAAGAAACGGTCAATGG 72
OY 115 CACGTTTTTTCATGGAAGCATTTTGGAAAAGCAATGTAATTTTGGAAACCAATTGATG 174
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 73 CACGAGTTTGAATATGAAGAGCGAAGAGAGGAGGCCATACGAAGGCCAATACCGTA 132
OY 175 CAATTCGGGTTACAAAGGAGTCCGTTGCCATTCGTTTCGATATTTGTTCCATAGCT 234
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 133 AAGCTTAAGTAAACCAAGGGGAGCTTTGCCATTTGCTTGGGATATTTTGTACACAAA 192
OY 235 TTCGAATACGGAATTCGCACTTTCACGAATATCCAGACGACATTCGGGACTACTTTGTT 294
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 193 TTTGACTATGGAAGCAAGCTATATGTCAAGCACCTGCCGACATACCACTATATAAAG 252
OY 295 CAATCATTCGCGGCTGATTTTCTTACGAAGAATCTATGCGTTTGAAGATGCGGCGCAT 354
```



```

OY 235 TTCCATACGGGATGCGACTTTACGAAATACCCAGAGCAGCATTCGGCACTATTGTT 294
    || || || || || || || || || || || || || || || || || || || || ||
DB 193 TTTCAGTATGAAACAGGATTTTTCACACACCTGACACATACATGATTTATTAAG 252
OY 295 CATCATTTCCCGCTGGATTTTCTACGAAAGAAATCTACGCTTTGAAGATGGCCATT 354
    || || || || || || || || || || || || || || || || || || || || ||
DB 253 CTCTCAATTTCCGAGGATATACATGGAAACGGTCCATGACCTTTGAAGCGGTGGCTTG 312
OY 355 GTTGCATTCGTTGAGATATACGTTAGAAAGATGATAGTTCATACAAAGTGGAGTAT 414
    || || || || || || || || || || || || || || || || || || || || ||
DB 313 TGTGTATATACCATGATGATATGAGTTTGACAGGCACTGTTTCTACTACGACATCAAGCTTC 372
OY 415 AGAGGCAACGGTTTCCCTAGTAACGAGCCGATGATCAAAAACCATCTCGGCATGAG 474
    || || || || || || || || || || || || || || || || || || || || ||
DB 373 ACTGCTTGAACGTTCTCCAAATGAGCCGTTGTGCAGAAAGAACACACTGGCTGGAA 432
OY 475 CCATGCTTTGAGTGGTCTACATGAAACAGCGGCTTGTGTGGGCAAGTAGATTCGTT 534
    || || || || || || || || || || || || || || || || || || || || ||
DB 433 CCGAGCAGCTGAGCGTTGATCTCTCGTGTGATGGTGTGATAGAGACATCCATCTGCT 492
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DB 453 CTGACAGTTGAAGAGAGTGCTGATTCAGCATGTGACATTAAGCTGTTTACAGGGCCAA 552
OY 595 GGTGAGTGAAGAAATTTCCGGAATATCACTTATTCATCATGCTGTGAGAAA--ACC 651
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DB 553 AAGCGCGCTTGAAGATGCGAGGATACATGTTGTTGACACCAAACTGTTATATGGAAC 612
OY 652 TACGTGAGAAAGAAAGCTTCTGTGGAACAACAGAGAGCGCCATTGCGAC 700
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DB 613 AACGACAAAGAAATTCATGAAGTTGAGAGCATGAATCGCCGTTGCGAC 661

RESULT 15
US-10-006-922-13
: Sequence 13, Application US/10005922
: Publication No. US20020197676A1
: GENERAL INFORMATION:
: APPLICANT: Lukyanov, Sergey A.
: APPLICANT: Fradkov, Arcady F.
: APPLICANT: Labas, Yulii A.
: APPLICANT: Matz, Mikhail V.
: TITLE OF INVENTION: No. US20020197676A1el Chromophores/Fluorophores and
: FILE REFERENCE: CLON-035CIP
: CURRENT APPLICATION NUMBER: US/10/006,922
: CURRENT FILING DATE: 2001-12-04
: PRIOR APPLICATION NUMBER: 09/120,330
: PRIOR FILING DATE: 1998-12-11
: PRIOR APPLICATION NUMBER: 09/457,898
: PRIOR FILING DATE: 1998-12-09
: PRIOR APPLICATION NUMBER: 09/458,144
: PRIOR FILING DATE: 1999-12-09
: PRIOR APPLICATION NUMBER: 09/458,477
: PRIOR FILING DATE: 1999-12-09
: PRIOR APPLICATION NUMBER: 09/457,556
: PRIOR FILING DATE: 1999-12-09
: PRIOR APPLICATION NUMBER: 09/444,338
: PRIOR FILING DATE: 1999-11-19
: NUMBER OF SEQ ID NOS: 46
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 13
: LENGTH: 696
: TYPE: DNA
: ORGANISM: Anemonia sulcata
US-10-006-922-13

Query Match 11.9% Score 131.4: DB 9: length 696:
Best Local Similarity 52.2% Pred No. 2.3e-22:
Matches 319: Conservative 0: Mismatches 286: Indels 6: Gaps 1:

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OY 65 TGAAGAGATTTCTGGCAAAAGCTAGCGTTGAGAGATCGTGAACAATCAGCTTTT 124

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OY 425 GTTTCCTAGTAAGGAGCCGATGATGCAAAAGCCATTCCTGCGCATGAGCCATGCTTTG 484
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OY 659 AAGAAGAGAGC 669
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DB 614 TTGAGAAAGCC 624

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Search completed: January 16, 2003, 15:01:54
Job time : 65.1814 secs

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

On nucleic - nucleic search, using sw model

(without alignments)
10652.486 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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5	392.6	36.4	1094	3	AY015995	AY015995 Piliostarc
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24	145.4	13.5	687	3	AF322221	AF322221 Anemonia
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ALIGNMENTS

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LOCUS	AX146235	1079 bp	DNA	linear
DEFINITION	Sequence 1 from Patent WO0134824.			
ACCESSION	AX146235			
VERSION	AX146235.1	GI:14284753		
KEYWORDS	.			
SOURCE	Renilla muelleri.			
ORGANISM	Renilla muelleri			
	Eukaryota; Metazoa; Anthozoa; Alcyonaria; Pennatulacea;			
	Sessiliflorae; Renillidae; Renilla.			
	1 (bases 1 to 1079)			
REFERENCE	Anderson, D.			
AUTHORS	Methods and compositions comprising renilla gfp			
TITLE				
JOURNAL	Patent: WO 0134824-A-1 17-MAY-2001;			

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DB	121	ACATAATATCTAAGAGACCGCTCATTTAAGAGTAGTAAATAATATATATGATAGAGTA	180
QY	181	TAAACTCTCGCCTTAGACAGACAGTGTGCAACAGACTACTCTGTATATGCAATCGAA	240
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DB	241	ACGCTAAGAGAGATTAAGATGATTAACAATATTGAAACAACCTGTTTATACAAAGATA	300
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DB	301	ATGTCGTATTAAGATAATCTGGAAGAAATTGTAACAACCACTGTTTATACATGGAAGGT	360
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DB	1021	TAAATTTTAAACAATTAATCAATGTTTGTGATATGTTGTAAAAAAAAAAAAAAA	1079
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LOCUS AX250573			
DEFINITION Sequence 15 from Patent WO0168824.			
ACCESSION AX250573			
VERSION AX250573.1 GI:J5984321			
KEYWORDS			
SOURCE			
ORGANISM			
Renilla muelleri.			
Eukaryota; Metazoa; Chordata; Anthozoa; Alcyonaria; Pennatulacea;			
Sessiliflorae; Renillidae; Renilla.			
REFERENCE			
Bryan, B.J., Szent-Gyorgyi, C. and Szecepaniak, W.			
Renilla reniformis fluorescent proteins, nucleic acids encoding the			
fluorescent proteins and the use thereof in diagnostics, high			
throughput screening and novelty items			
Patent: WO 0168824-A 15-20-SEP-2001;			
Prolume, Ltd. (US); Bryan, Bruce J. (US)			
JOURNAL			
location/Qualifiers			
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DB	1	GGTTATACACAAAGTATGCGCGTATCTGCAGACGATCTAGTGGATTATTGCGAGCGGTA	60
QY	61	GTAATTACGTCAGACCTGCTCTAATCCAAACCAAACTCTTAAATTAAGCAGACATTT	120
DB	61	GTAATTACGTCAGACCTGCTCTAATCCAAACCAAACTCTTAAATTAAGCAGACATTT	120
QY	121	ACATAATATCTAAGAGACCGCTCATTTAAGAGTAGTAAATAATATATATGATAGAGTA	180
DB	121	ACATAATATCTAAGAGACCGCTCATTTAAGAGTAGTAAATAATATATATGATAGAGTA	180

OY	554	CATTACGCTTACCAACATGGCGGACCTGTTGAAATTCGTCCAGATATTAATTTAAATAGAAAG	613
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OY	674	TGCAGAGACTATCTTAGCAATAGAGCCCTTCATTTGAAAGCCATGTACATGAATTAATGGCG	733
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RESULT 4			
AR151730			
LOCUS	AR151730	1085 bp	DNA linear PAT 08-AUG-2001
DEFINITION	Sequence 15 from patent US 6232107.		
ACCESSION	AR151730		
VERSION	AR151730.1	GI:15117780	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1085)		
AUTHORS	Bryan,B.J. and Szent-Gyorgyi,C.		
TITLE	Luciferases, fluorescent proteins, nucleic acids encoding the luciferases and fluorescent proteins and the use thereof in diagnostics, high throughput screening and novelty items		
JOURNAL	Patent: US 6232107-A 15-15-MAY-2001;		
FEATURES	Location/Qualifiers		
source	1..1085		
BASE COUNT	376 a 176 c 209 g 320 t 4 others		
ORIGIN	/organism="unknown"		
Query Match	98.4%;	Score 1061.4;	DB 6; Length 1085;
Best Local Similarity	99.4%;	Pred. No. 1e-221;	
Matches 1078:	Conservative 0;	Mismatches 1;	Indels 6; Gaps 1;
OY	1	GGTTATACAGAGCTGTATCGCGCTATCTCGACAGCGGATCTAGTGGGATTAATTCGACGGGTA	60
Db	1	GGTTATACAGAGCTGTATCGCGCTATCTCGACAGCGGATCTAGTGGGATTAATTCGACGGGTA	60
OY	61	GTAATTACGTCAGACCTGTCTAATCGAAACCCACACAAACTCTTAAATTAACCCACATTT	120
Db	61	GTAATTACGTCAGACCTGTCTAATCGAAACCCACACAAACTCTTAAATTAACCCACATTT	120
OY	121	ACAATAATCTTAAGAGACGCGCTCAATTAAGAGTAGTAAAAATATATATGATGAGACTA	180

Db	121	ACATATATTTCTAAGAGACGCCCTCATTTTAAGCTAGTATAAAATATATATATATATAGTATAGCTA	180
Oy	181	TACAACTCTGCGCCTTAGACAGACAGACTGTGGCAACAGAGTAACCTCTTGTTAATGCATCGAA	240
Db	181	TACAACTCTGCGCCTTAGACAGACAGACTGTGGCAACAGAGTAACCTCTTGTTAATGCATCGAA	240
Oy	241	AGCGCAAGACAGATTAACATGATGATTAACCAAAATATGGAAGAACACTGTGTTACAGAACTA	300
Db	241	AGCGCAAGACAGATTAACATGATGATTAACCAAAATATGGAAGAACACTGTGTTACAGAACTA	300
Oy	301	ATGTGCTATTAAGTAAATCTGGAGGAATTTGTAACAACCAATGTTTTTATCAATGGAGGGT	360
Db	301	ATGTGCTATTAAGTAAATCTGGAGGAATTTGTAACAACCAATGTTTTTATCAATGGAGGGT	360
Oy	361	TGCGGCAAAAGGGAATATTTTTATTGCGCAATCAACTGTGTTACAGATTCGTGTCACGAAAGG	420
Db	361	TGCGGCAAAAGGGAATATTTTTATTGCGCAATCAACTGTGTTACAGATTCGTGTCACGAAAGG	420
Oy	421	GGCCCACTGCGCTTTTGCAATTTGATATTTGTGTACACAGCTTTTCAATATGGCAACCGTACT	480
Db	421	GGCCCACTGCGCTTTTGCAATTTGATATTTGTGTACACAGCTTTTCAATATGGCAACCGTACT	480
Oy	481	TTACAGGAATATCCGATATGATATATACATTAATTTTATACATCAATCTTTCCAGAGATTT	540
Db	481	TTACAGGAATATCCGATATGATATATACATTAATTTTATACATCAATCTTTCCAGAGATTT	540
Oy	541	ATGTATGAACGACAACTTACGTTACGAAGATGGCGACTTGTGGAATTCGTTACAGATATA	600
Db	541	ATGTATGAACGACAACTTACGTTACGAAGATGGCGACTTGTGGAATTCGTTACAGATATA	600
Oy	601	AATTTAATAGAAGACAACTTGTCTACAGAGTCCGAATACAAAGTATGTAACCTTCCACAT	660
Db	601	AATTTAATAGAAGACAACTTGTCTACAGAGTATCAAAAGTATGTAACCTTCCACAT	660
Oy	661	GATGTCGCCGTCATGCAGAAAGACTTCTTAGAATATAGAGCCCTGATTTGAAGCCATGTAC	720
Db	661	GATGTCGCCGTCATGCAGAAAGACTTCTTAGAATATAGAGCCCTGATTTGAAGCCATGTAC	720
Oy	721	ATGAATTAATGGCGTCTTGGTGGCGCAAGTAAATCTTGTCTATAAATACTCTGGGAAA	780
Db	721	ATGAATTAATGGCGTCTTGGTGGCGCAAGTAAATCTTGTCTATAAATACTCTGGGAAA	780
Oy	781	TATTTATTCATGTACATATAAAACATTAAATGAAGTGAAGGTGTAGTAAAGAGTTTCTT	840
Db	781	TATTTATTCATGTACATATAAAACATTAAATGAAGTGAAGGTGTAGTAAAGAGTTTCTT	840
Oy	841	TGCTATCAATTTTATTTCAACATCGTTTGGAAAAAGACTTACGTAGAAGACGGGGGGTTCGTT	900
Db	841	TGCTATCAATTTTATTTCAACATCGTTTGGAAAAAGACTTACGTAGAAGACGGGGGGTTCGTT	900
Oy	901	GAACAGCATGAGACGTGATTTGCTCAATATGCATATATAGGAAAAACCACTAGATCTTTA	960
Db	901	GAACAGCATGAGACGTGATTTGCTCAATATGCATATATAGGAAAAACCACTAGATCTTTA	960
Oy	961	CACGAATGGGTTTAAACACAGTTACATTACTTTTCCAAATTCGTTTCATGTCAAAATAA	1020
Db	961	CACGAATGGGTTTAAACACAGTTACATTACTTTTCCAAATTCGTTTCATGTCAAAATAA	1020
Oy	1021	T-----AATTTTTTAAACAATATATCAATGTTTTGTATGTGTTTGTAAAAA	1074
Db	1021	TATTTTAAATATTTTAAACAATATATCAATGTTTTGTATGTGTTTGTAAAAA	1080
Oy	1075	AAAAA 1079	
Db	1081	AAAAA 1085	

VERSION	AT015995.1	GI:12621057
KEYWORDS	Ptilosarcus sp. CSC-2001.	
SOURCE	Ptilosarcus sp. CSC-2001	
ORGANISM	Eukaryota; Metazoa; Chordata; Anthozoa; Alcyonaria; Pennatulacea; Subselliflorae; Pennatulidae; Ptilosarcus.	
REFERENCE	1 (bases 1 to 1094)	
AUTHORS	Szent-Gyorgyi,C.S. and Bryan,B.J.	
TITLE	Luciferases, fluorescent proteins, nucleic acids encoding the luciferases and fluorescent proteins and the use thereof in diagnostics, high throughput screening and novelty items	
JOURNAL	Parent: US 6232107-B-15-MAY-2001; Prolume Ltd.; 1085 William Pitt Way, Pittsburg, PA; USA.	
REFERENCE	2 (bases 1 to 1094)	
AUTHORS	Szent-Gyorgyi,C.S. and Bryan,B.J.	
TITLE	Direct Submission	
JOURNAL	Submitted (07-DEC-2000) Prolume Ltd., 1085 William Pitt Way, Pittsburg, PA 15238, USA	
FEATURES	Location/Qualifiers	
source	1..1094	
gene	/organism="Ptilosarcus sp. CSC-2001"	
	/db_xref="taxon:148367"	
	1..1094	
	/gene="GFP"	
	24..740	
CDS	/gene="GFP"	
	/product="green fluorescent protein"	
	/protein_id="AA054097.1"	
	/translation="MNRVNLKNTDLKEIMSKASVEGITVNNHVESMEGFGKGVNLGN	
	OLMORVHTKGGPLPAPFIVISLAPYQGNRTPTKPDIDVDFVPSFAGFVEYERNLRF	
	EDGALVDIRSDISLEDDKFEHKKVEYRGKGFSGNSGPNOKALICKEPSFEVYNNISGLV	
	VGEDVLYRKLESGNYSCMKTFYFRSKGVGPEPEYHFIHRLKTEVEGSPVEQHE	
	TAIADLTITGRPLGSLHEWV"	
BASE COUNT	358 a 212 c 253 g 291 t	
ORIGIN		
Query Match	36.4%; Score 392.6; DB 3: Length 1094;	
Best Local Similarity	71.3%; Pied. No. 1; 2e-75;	
Matches 518: Conservative	0; Mismatches 209; Indels 0; Gaps 0;	
QY	252 AGATAGATGACTTAACAATATTTGAAGAACACTGTTTACANGAGTATGTCGTATTA	311
Db	17 AGACAATATGACCCGACACTATTAAAGAACACTGACGTAAGAGATATGTCCGCAA	76
QY	312 AGTAATCTGGAAGGAAATTTAACAACCATGTTTACATATGGAGGGTTGGCGAAG	371
Db	77 AGTAGCGTTGAAGGATCGTGAACATACAGTTTTTTCATATGGAAGATTGGAAAG	136
QY	372 GAATATTTTATTCGGGCATCACTGGTTCAGATTCGTGTACAGAAAGGCGCCCACTGC	431
Db	137 CAATGTATTTTTCGGAACCAATTCGATGCAATCCGGGTTACAAAGGAGGTCGTTGCC	196
QY	432 TTTTGCAATTTGATATGTGTACACAGCTTTTCAATATATGACACCGTACTTTCACGAAATA	491
Db	197 ATTGCGTTTCGATATTCGTTTCATAGCTTTTCAATCAATCGGAAATCGCACTTTCACGAAATA	256
QY	492 TCGCAATGATATATCAGATTATTTTATACATATTTCCAGCGAGATTTATGATATAGC	551
Db	257 CCCAGACGACATTCGGACTACTTTTGTTCATATATTCGCCGCTGGAATTTTTCAGCAAG	316
QY	552 AACATTTACGTTACAGAGATGGCGGACTGTTTGAATTCGTTACGATATATAATTTAATA	611
Db	317 AAATCTACGCTTTGAGATGGCGGCATTTGTGCAATTCGTTACGATATATAAGTTTAAAGA	376
QY	612 AGACAAGTTGCTTACAGAGATCGAATCAAAAGGAGTAACTTCCCGAGATGATGTCGCCG	671
Db	377 TGATTAAGTTCACATCAAAAGTGAGAGTATAGAGGACACGCTTTCCTTAGTAACGACCCGT	436
QY	672 CATCGAAGACTATCTTAGATATAGAGCCCTTCATTTTGAACCATGTACATGATTAATGG	731

Db	437	GATGCAAAAAGCCATCTCTCGGCATGAGACCATCTTTGAGTGGTCTTACATGAAACAGCG	496
Qy	732	CGTCTGGTCGGCCGAAGTAATTTCTGTCTATAACTCTAGCAACTCTGGGAAATATATTCATG	791
Db	497	CTTTCTGGTGGCCAGAGTAGATCTTCGTTTACAACTCGAGTCAGGAAACATATTCCTG	556
Qy	792	TCACATGAAAACATTAATGAAGTGCAGAAAGGTGTAGTAAGAGTTTCTTCGTATCATTT	851
Db	557	CCACATGAAAACGTTTACAGATCCCAAGAGGTGAGATGAAGAAATTCGCCGAATATCATTT	616
Qy	852	TATTCACATCTGTTTGAAGAAAGACTTACGTAGAACGCGGGGTTCGTTGAACAGCATGA	911
Db	617	TATTCATCTCTCTCTCGAGAAAACCTAGCTGAGAACAGAAAGAGTTCTGTGGAACAACAGA	676
Qy	912	GACTCTATTGCTCAATATGACATCTATAGAAAACCACTAGATCTCTTACACAGATGGCT	971
Db	677	GACGGCATTTGCACAACGTGACCACTGCAATTGGAAACCTCTGGGCTTCCTTCATGAAATGGT	736
Qy	972	TTAACA 978	
Db	737	GTAAGAA 743	
RESULT 6			
AR151735		1104 bp	DNA
LOCUS	AR151735		linear
DEFINITION	Sequence 30 from patent US 6232107.		PAT 08-AUG-2001
ACCESSION	AR151735		
VERSION	AR151735.1		GI:15117785
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1104)		
AUTHORS	Bryan,B.J. and Szent-Gyorgyi,C		
TITLE	Luciferases, fluorescent proteins, nucleic acids encoding the		
	luciferases and fluorescent proteins and the use thereof in		
	diagnostics, high throughput screening and novelty items		
JOURNAL	Patent: US 6232107-A 30 15-MAY-2001;		
FEATURES	Location/Qualifiers		
source	1..1104		
BASE COUNT	360 a 215 c 237 g 292 t		
ORIGIN			
Query Match	36.4%; Score 392.6; DB 6; Length 1104;		
Best Local Similarity	71.3%; Pred. No. 1.2e-75;		
Matches 518; Conservative	0; Mismatches 209; Indels		0.
Qy	252	AGATAGATAGATGAATCAAAATATTGAAGACACTGTTTACAGAAGTATGTCGTATTA	311
Db	27	AGACAAAATGACCCGACGCTATTTAAAGAACCTGACGTGAAGAGATTTATGTCGCCAA	86
Qy	312	AGTAATCTGGAAGGAATTTAAACAACCATGTTTTTACATGAGAGGCTTCCGCAAGG	371
Db	87	AGTAGCGTTGAAGAGATGCTGAACATCACTGTTTTTTCATGGAAGGATTTGSAAGG	146
Qy	372	GAATATTTTATTCGGCATCACTGCTCGAGTTTCGTACAGGAAGGGGCCACATGCC	431
Db	147	CAATGTATTTATTCGAACAACCATGATGCAAAATCCGGGTTACAAAGGAGGCTCCGTTGC	206
Qy	432	TTTTCATTTGATTTTGTGTCACGACCTTTTCATATGCGACACCGTACTTTCCAGAAATA	491
Db	207	ATTGCTTTTCATATTTGTTTTCATAGCTTTCCAAATACGGGATGCGACTTTCACAGATA	266
Qy	492	TCGCAATGATATACAGATTATTTTATACATCACTTTCCAGCAGAGATTTATGATGAGC	551
Db	267	CCCGAGACGACATTCGCGACTTCTGTTTCATCTATTCGCCGCTGAGATTTTCTAGCAAG	326
Qy	552	AACATTTAGCTAGCAAGATGCGGCACTGTTGGAATTCGTTCAAGATTTAAATTTAATGA	611
Db	327	AAATCTACGCTTTGAAGATGCGGCATTTGTTGACATTCGTTCAAGATTTAAGTTAGAGA	386

OY	612	AGCAGGATTCGTACAGAGTGCATAACAAAGTAGTAACCTTCCAGANGATGGTCCCGT	671
Db	387	TGATAAGTTCACCTACAAGAATTGAGATATAGAGCAACGGTTTCCCTAAGAACGGACCGCT	446
OY	672	CATGCAAGAGACTATCTWAGSAATAGAGCTTCATTGSAAGCCATCTACATGAATAAATG	731
Db	447	GATGCCAAAAGGCATTCCTGGCATGAGCGCATCTGTTTGAGTGGCTGTACATATGAACGACGG	506
OY	732	CGTCTTGGTGGCGCAAGTAATTCCTGTCTATAAACTAACTGGGAAATATATATTCATG	791
Db	507	CGTTTGGTGGCGCAAGTAGATCTCGTTTACAACATCGAGTCAAGGAACTATATACCTG	566
OY	792	TCACATGMAAAACATTATATGAAGTCCAAAGGCTAGTAAGAAGATTCTCGTATCATTT	851
Db	567	CCACATGMAAAACGTTTTACGATCCCAAAGGTGAGGAAGAAATTCGCCGAAATATCATTT	626
OY	852	TATTTAACATCTGTTGGAAAAAGACTTACGTAGTAAGAAGCGGGGGTTCGTTGAACAGCATTA	911
Db	627	TATTCATCATCTGCTTCGGAGAAAAACCTACCTGGAAAGGAAGAACTTCGTGGAACAACACGA	686
OY	912	GACTGCTATTGGCTCAATGACATCTATATAGAAAAACCATAGAGTCTTACACGAATGGGT	971
Db	687	GACGGCCATTTGACACAACATGACCAACAATTGGAANAACCTCTGGGCTCCCTTCATGAATGGGT	746
OY	972	TTAAACA	978
Db	747	GTAGAA	753

RESULT 7				
AX146237				
LOCUS	AX146237	1104 bp	DNA	linear
DEFINITION	Sequence 3 from Patent WO0134824.			PAT 31-MAY-2001
ACCESSION	AX146237			
VERSION	AX146237.1	GI:14284755		

SOURCE	1. Pilosarcus gunneyi. Pilosarcus gunneyi
ORGANISM	Eukaryote; Metazoa; Chordata; Anthozoa; Alcyonaria; Pennatulacea; Subselliflorae; Pennatulidae; Pilosarcus.
REFERENCE	1 (bases 1 to 1104)
AUTHORS	Anderson,D.
TITLE	Methods and compositions comprising renilla gfp
JOURNAL	Patent: WO 0134824-A 3 17-MAY-2001; Rigel Pharmaceuticals, Inc. (US)
FEATURES	location/Qualifiers
source	1..1104
	/organism="Pilosarcus gunneyi"
	/db_xref="taxon:161601"
BASE COUNT	360 a 215 c 237 g 292 t
ORIGIN	

[illegible]

Db	267	CCCGAGCGACATTCGGGACTACTTTGTTCAATTATTCGCCGGCTGGATTTTCTACGCAAG	326
QY	552	AACATTACGTTACGAGATGCGGAGCTTGTGAAATTCGTTCAGATATAAATTTAAATAGA	611
Db	327	AAATCTACGCTTTGGAAGATGGCCCAATTCGTGACATTCGTTGAGATATATGAATTTACAGA	386
QY	612	AGACAGTTTCGTTACAGAGATCCAAATACAAAGGTAGTAACTTCCCGAGATGATGGTCCGGT	671
Db	387	TGATAGTTCCACTACAAAGTGGAGTATAGAGCCAAAGGTTTCCATAGTACGACACCGGT	446
QY	672	CATCGAGAGACATATCTTGGAATTACAGCTTCATTTGAAACCATATACATGATATATGG	731
Db	447	GATGCAAAAAGCCATCTCGTGATGGAGCCATCTGTTGGAGTGCTGTACATGAAACAGCGG	506
QY	732	CGTCTTGGTGGCGAAGTAAATCTTGTCTATAACTAACTCGGGAATATATATTCATGG	791
Db	507	CGTTCTGGTGGCGAAGTAAATCTGTTTACAACTCGAGTACGGAACATATTACTCGGG	566
QY	792	TCACATGAAGAACTTATATGAGTCGGAAGCTGTAGTAAAGGATTTCTTCGTATCATTT	851
Db	567	CCACATGAAGAACTTTTACAGATCCAAAGGTGAGGAAGATATTCGCCGAATATCATTT	626
QY	852	TATTTCAACATCTTTGGAAAGACTTAGCTAGAGACGCGGGGTTTCGTTGAACAGCATGA	911
Db	627	TATTCATCATCTCTCGAGGAAAACTTACTGGAAGAGAACTTCGTGGAACAACACGA	686
QY	912	GACTCTATTTGTCAAATGACATCTATATGGAAACCACTAGATATCTTATACAGATGGGT	971
Db	687	GACGCGCATTTGCACACAGCTGACCACCAATTTGGAATAACCTCTGGGGCTCCCTTCATGATGGGT	746
QY	972	TTTAAACA	978
Db	747	GTAGAA	753

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RESULT 8
AX250588
LOCUS
DEFINITION
Sequence 30 from Patent WO0168824.
AX250588
ACCESSION
AX250588.1 GI:15984339
VERSION
KEYWORDS
SOURCE
ORGANISM
Ptilosarcus gurneyi.
Ptilosarcus gurneyi
Eukaryota; Metazoa; Chnidaria; Anthozoa; Alcyonaria; Pennatulacea;
Subsiliiflorae; Pennatulidae; Ptilosarcus.
1 (bases 1 to 1104)
Bryan,B.J., Szent-Gyorgyi,C. and Szecepaniak,W.
Renilla reniformis fluorescent proteins, nucleic acids encoding the
fluorescent proteins and the use thereof in diagnostics, high
throughput screening and novelty items
Patent: WO 0168824-A 30 20-SEP-2001;
Prolume, Ltd. (US) ; Bryan, Bruce J. (US)
location/Qualifiers
1..1104
/organism="Ptilosarcus gurneyi"
/db_xref="taxon:161601"
34..750
CDs

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Query Match	Score	392.6	DB 6	Length	1104
Best Local Similarity	71.3%	Prod No	1 2a-25		
<p> <code>/note="Ptilosarcus Green Fluorescent Protein"</code> <code>/cdon_start=1</code> <code>/protein_id="CAC93791.1"</code> <code>/db_xref="GI:15984340"</code> <code>/translation="MNRNVLKNTGLKEIKMSAKASVEGI VNNHVFSEMGFGKGNVLFGN</code> <code>QMGQIVFTKGGPLPEAFEDIVSAFOYGNFTPIKYPDDIADYEVQSPFAGEFYERNLRF</code> <code>EGGATIVDSIDSLDEDDKPHYKVEYKNGNCFPSGPMQAKAILGMKPSPEVYVNNSSVL</code> <code>VEEDIVLVKLTESGNYSCMKMTFRRSGVKREPEYHFTIHKLEKTYVEEGSTFDOHE</code> <code>YIAQITTTGKPLGSIHEWV"</code> </p>	360 a	215 c	237 g	292 t	
BASE COUNT					
ORIGIN					

	Matches	518: Conservative	0: Mismatches	209: Indels	0: Gaps	0:
QY	252	AGATTAGATGAGTAAACAAATATTGAGACACACTTTGTTTACAGAGTAATGTGCTATAA	311			
Db	27	AGACAAATATGACCCCAACGTAATTAAAGACACTGGACTGAAAGATATTATGTGGGAAA	86			
QY	312	AGTAAATCGTAGAGCAATTTGTAACCAACACTGTTTTCATATGGAGGGTCCGGCAAG	371			
Db	87	AGCTAGCGCTTGAGGAATTCGTGAAACAATCACGTTTTTTCCATGGAAAGATTTGGAAAAAG	146			
QY	372	GAAATTTTATTCGGCAATTCAACTGGTTCCAGATTGCTGTCAAGAAAGGGGCCCACTGCC	431			
Db	147	CAATGCTATTATTTGGAAACCAATTGATCAATTCGAGTTCACAAAGGAGAGTCCGTTGCC	206			
QY	432	TTTTGCATTGTAATTGTGTCAACGCTTTTCAATATGGCAACGTACTTTCCAGGAATA	491			
Db	207	ATTCCCTTTGGATATTGTTTCCATAGCTTTCCAAATACGGGAATGCACTTTACAGAAATA	266			
QY	492	TCCGATGATATATCAGATTATTTATTCAAATCATTTCCACAGAGATTATATATGAAG	551			
Db	267	CCCAGACGACATTTGGGGACTACTTTGTTCAATCATTTCCGGCTGGATTTTCTACGAAG	326			
QY	552	AACATTACGTTACGAAGATGGCGGACTGTGGAATTGCTTCAGATATTAATTTAATAGA	611			
Db	327	AAATCATACCTTTGAAGATGCGCCACTTTGTGACATTGTTACAGATATTAAGTTTAAGA	386			
QY	612	AACACAAGTTCGCTCAAGAGTGCATACAAAGGTGTAACTTCCAGATGATGGTCCGT	671			
Db	387	TGATATATCTCACTCAAAAGTGGAGTATAGAGCAACGCTTTCCCTACTAACGACCCCT	446			
QY	672	CATGCGAGAACACTATCTTAGAATAGAGCTTCATTTGAAGCCATGATCATGAATATATGG	731			
Db	447	GATCGAAAAGGCAATCTCGGCTGAGACCATCGTTTAGAGTGCTCTACATGAAACGGG	506			
QY	732	CGCTTTGCTGGCGGAAGTATTTCTGTATTAACCTAACTCTGGGAAATATTATTAAG	791			
Db	507	CGTTCTGGGCGCAAGTATGATCTCGTTTACAACTCGAGTACGGGAACATACTACTCGTG	566			
QY	792	TCACATGAAGAACTTATATGAAAGTCGAAGGTAGTAAAGGATTTCTTCGTATCATTT	851			
Db	567	CCACATGAAGAACTTTTACAGATCCAAAGAGTGGAGTGAAGAAATTTCCGGAAATATCATTT	626			
QY	852	TATTCAACTCGTTTGGAAAAGACTTACTAAGAAAGCGGGCTTCGTTGAACACACATGA	911			
Db	627	TATCCATCATCTGCTGGAAAAAACCTTACGTGGAAGAGAAAGCAACTCTGTGGAACAACAGA	686			
QY	912	GACTGCTATTGTCATATGACATCTTATAGGAAGCACTAGAGATCTTTACAGAAATGGGT	971			
Db	687	GACGCGCATTTGCACACACTGACCAATTTGCAAAAACCTCTGGGCTCCCTTCATGAATGGT	746			
QY	972	TTAACA 978				
Db	747	GTAGAAA 753				
RESULT 9						
AR151736						
LOCUS	AR151736	1279 bp	DNA	linear	PAT 08-AUG-2001	
DEFINITION	Sequence 31 from patent US 6232107.					
ACCESSION	AR151736					
VERSION	AR151736.1	GI:15117786				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 1279)					
AUTHORS	Bryan,B.J., and Szent-Gyorgyi,L.C.					
TITLE	Nucleases, fluorescent proteins, nucleic acids encoding the					
	nucleases and fluorescent proteins and the use thereof in					
	diagnostics, high throughput screening and novelty items					
JOURNAL	Patent: US 6232107-A 31 15-MAY-2001;					
FEATURES	Location/Qualifiers					
source	1..1279					

BASE COUNT	449 a	234 c	263 g	333 t	
ORIGIN	/organism="unknown"				
Query Match	36.3%; Score 391.6; DB 6; Length 1279;				
Best Local Similarity	71.2%; Pred. No. 2e-75;				
Matches	517; Conservative 0; Mismatches 209; Indels 0; Gaps 0;				
QY	253	GATTAAGATGAGTAAACCAATATATGGAAGAACCTGTTTACAGAGAATATGCTGATAAA	312		
Db	1	GACAAATGAACCCGACACGATATTTAAAGAACCTGACCTGAAAGAGATTTATGCGCAAAA	60		
QY	313	GTAATCTGGAAGAAATGTAAACACCATGCTTTTACATGAGAGGTTGCGGCAAAAGG	372		
Db	61	GCTACCGTTGAAGGAATCGTAGCAATACCGTTTTCATGGAAGCATTTGGAAGAGC	120		
QY	373	AATATTTTATTCGGCAATACACTGGTTCAGATTCGTCGACGAAAGGGGCCCGCTGCT	432		
Db	121	AATGATATATTTTGGAAACCAATGATGCAAAATCCGGTTTACAAAGGGAGTCCGTTGCCA	180		
QY	433	TTTGATTTGATTTGTTGTGTCACACCTTTTCATATTTGCAACCCGACTTTCACGAAATAT	492		
Db	181	TTTCGCTTCGACATTTGTTTCCATACCTTTCCATATCGGGAATTCGACTTTCACGAAATAC	240		
QY	493	CCGAATGATATATTCAGATTTATTTATACAAATTCATTCACAGCAGATTTATGATGACGA	552		
Db	241	CCAGACGACATTTGCGGACACTTTTTCATATTCATTTCCGGCTGGATTTTTCACCAAGA	300		
QY	553	ACATTAACCTTACGAGATGCGGACCTGTTGAAATTTGTCGATATTAATTAATTAAGAA	612		
Db	301	AATCTAGCTTTGAAGATGCGCCCATTTGTGACATTCCTTCAGATATTAAGTTTAGAAGAT	360		
QY	613	GACAACTTGCTACAGACTGCAATACAAAGGTAGTAACCTCCAGATGATGCTCCGCTC	672		
Db	361	GATTAATCTCCATACAAATGGAGTATAGAGCAACGGTTTTCCTAGTACGACCGACCGTG	420		
QY	673	ATGCGAAGACATATCTTTAGCAATFAGAGCCCTCATTTTGAAGCCATGACATGATATGAC	732		
Db	421	ATGCAAAAAAGCCATCTCGGCAATGGAGCCATGCTTTGAGGTGCTTACATGCAACAGCGGC	480		
QY	733	GTTCTGGTGGGGAAGTAAATTTCTGTCTATTAACATAACTTGGGAATATTATTATCATGT	792		
Db	481	GTTCTGGTGGGGAAGTAAATTTCTGTCTATTAACATAACTTGGGAATATTATTATCATGT	540		
QY	793	CACATGAAAAACATTAATGAAGTCGAAGGTGATGAAGACGATTTCTTCGATCATTTT	852		
Db	541	CACATGAAAAACGTTTACGATGTCAAAGGTGAGTGAAGAAATTCGCCGAAATATACATTT	600		
QY	853	ATTCAACATCTGTTTGGAAAAAGACTTACGTAGAGAAGAGGGGGTTCGTTGAACGAGCATGAG	912		
Db	601	ATCATCATCATCTGTGGAAGAAACCTGAGGAAGGAAGAAAGTCTGTCGACACACACAGG	660		
QY	913	ACTGCTATTGCTCAATGACATCTATAGAAAAACCACTAGATCTCTTACACAAATGGGTT	972		
Db	661	ACCGCATTTGACACACTGACACCAATTTGCAAAACCTTCGGGCTCCCTTCATGATATGGGTG	720		
QY	973	TAAACA 978			
Db	721	TAGAAA 726			
RESULT 10					
LOCUS	AX146238	1279 bp	DNA	linear	PAT 31-MAY-2001
DEFINITION	Sequence 4 from Patent W001334824.				
ACCESSION	AX146238				
VERSION	AX146238.1	GI:14284756			
KEYWORDS					
SOURCE	Ptiliosarcus guineyi.				
ORGANISM	Ptiliosarcus guineyi.				
	Eukaryota; Metazoa; Chnidaria; Anthozoa; Alcyonaria; Pennatulacea;				
	Subellilliflorae; Pennatulidae; Ptiliosarcus.				
REFERENCE	1 (bases 1 to 1279)				

AUTHORS Anderson, D.
TITLE Methods and compositions comprising renilla gfp
JOURNAL Patent: WO 0134824-A 4 17-MAY-2001;
Rigel Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source 1. 1279
/organism="Ptiliosarcus gurneyi"
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7-723
CDS /note="unnamed protein product"
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BASE COUNT 449 a 234 c 263 g 333 t
ORIGIN

Query Match 36.3%; Score 391.6; DB 6; Length 1279;
Best Local Similarity 71.2%; Pred. No. 2e-75;
Matches 517; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

OY 253 GATAAGATGAGTAAACAATATTGAAGACACATGTTTACAGAGATGCTGTATAA 312
DB 1 GACAAATGGAACCGCAGCATATTAAAGACACTGGACTGAAAGAGATTATGTGGCAAAA 60
OY 313 GTAATCTGGAAGGAAATTTGAACCAACCATGTTTTCATGAGAGGGTGGCCAAAGG 372
DB 61 GCTAGCGTTGAGAAACGTAACCAATCAACGTTTTCATGAGAGGATTGGAAAAAGC 120
OY 373 AATATTTTATGGGCATCACTGGTTCAGATTCGTCTCACGAAAGGGGCCCACTGCC 432
DB 121 AATGTATTATTGGAAACCAATTGACAAATCCGGGTTACAAAGGAGGTCGGTCCCA 180
OY 433 TTTGCATTGATATTGTGTACCCAGCTTTTCAATATGCGAACCGCTTTCACGAATAT 492
DB 181 TTGCGTTTCAGCATGTTTTCATAGCTTTTCATAGCGGAGATGCGACTTTCACGAATAT 240
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DB 241 CCGAGACATTTGCGGACATCTTTGTTCATCTTTCCGGCTGAGTTTTCACGAAGA 300
OY 553 ACATTACGTACGAAGATGCGGACTTTGTAAGATTCGTTCAGATATTAATTAATAGA 612
DB 301 AATCTACGCTTTGAGATGGCGCATTTGTGACATTTCGTTCAAGATATTAAGAT 360
OY 613 GACAGTCTGCTACAGAGTGCATCAAAAGTAGTAACTCCAGATGATGTCCTCCGTC 672
DB 361 GATTAAGTTCACATCAAAATGGAGTATAGAGCAACGTTTCCCTAGTAACGACCCG 420
OY 673 ATGACAAGACATCTTAGAATAGAGCCTTCATTTGAAGCCATGATGATTAATAGGC 732
DB 421 ATGCAAAAAGCCATCTCGGACATGAGCCATGTTTGAAGTGGTCTTCAACCAACGCG 480
OY 733 GTCTTGGTGGGAGGAAATTTCTGTCTATAAATTAACCTGGGAAATATTAATTCATG 792
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OY 853 ATTCAACATCGTTTGGAAAGACTTACGTAAGAACGGGGGTTGTTGAACAGCATGAG 912
DB 601 ATTCATCATCTGCTGGAGAAACCTACGTAAGGAAAGGAAAGCTTCGTGGAACACGAG 660
913 ACTGCTATTGCTCAATGACATCTATAGGAAACCACTAGATTCCTTACACCAATGGGTT 972
661 ACGGCATATGCAACACTGACCAACATTTGGAACCACTCTGGGCTCCCTTCATGATAGGGTG 720

OY 973 TAAACA 978
DB 721 TAGAAA 726

RESULT 11
AX250589
LOCUS AX250589 1279 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 31 from Patent WO0168824.
ACCESSION AX250589
VERSION AX250589.1 GI:15984341
KEYWORDS
SOURCE
ORGANISM Ptiliosarcus gurneyi.
Ptiliosarcus gurneyi
Eukaryota; Metazoa; Chnidaria; Anthozoa; Alcyonaria; Pennatulacea;
Subphylum: Pennatulidae; Ptiliosarcus.
1 (bases 1 to 1279)
Bryan, B.J., Szent-Gyorgyi, C. and Szczepaniak, W.
Renilla reniformis fluorescent proteins, nucleic acids encoding the
fluorescent proteins and the use thereof in diagnostics, high
throughput screening and novelty items
Patent: WO 0168824-A 31 20-SEP-2001;
Protime, Ltd. (US); Bryan, Bruce J. (US)
location/Qualifiers
1. 1279
/organism="Ptiliosarcus gurneyi"
/db_xref="taxon:161601"
7. 723
CDS /note="Ptiliosarcus Green Fluorescent Protein (GFP)"
/codon_start=1
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/db_xref="GI:15984342"

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. 1279
/organism="Ptiliosarcus gurneyi"
/db_xref="taxon:161601"
7. 723
CDS

Query Match 36.3%; Score 391.6; DB 6; Length 1279;
Best Local Similarity 71.2%; Pred. No. 2e-75;
Matches 517; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

OY 253 GATAAGATGAGTAAACAATATTGAAGACACCTTTTACAGAGATGCTGTATAA 312
DB 1 GACAAATGGAACCGCAGCATATTAAAGACACTGGACTGAAAGAGATTATGTGGCAAAA 60
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OY 433 TTTGCATTGATATTGTGTACCCAGCTTTTCAATATGCGAACCGTACTTTACGAATAT 492
DB 181 TTGCGTTTCAGCATGTTTTCATAGCTTTTCATAGCGGAGATGCGACTTTCACGAATAT 240
OY 493 CCGAATGATATACATATTATTATACATATTCAGCAGAGATTATATATAGAACGA 552
DB 241 CCGAGACATATTGGCGACTACTTTTCAATCATTTTCCGGCTGGATTTTTCACGAAGA 300
OY 553 ACATTACGTTACGAAGATGCGGACTTGTGAATTCGTTTCAGATATTAATTAATAGA 612
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OY 613 GACAGTCTGCTACAGAGTGCATCAAAAGTAGTAACTCCAGATGATGTCCTCCGTC 672
DB 361 GATTAAGTTCACATCAAAATGGAGTATAGAGCAACGTTTCCCTAGTAACGACCCGTG 420
OY 673 ATGCAAGACATATCTTAGAATAGAGCTTCATTTGAAGCATGATGATTAATAGGC 732

Db	421	ATGCAAAAGCCATCTCTCGGCATGGAGGCATCGTTTGAGGTGCTTACATGAAACGGCGC	480
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OY	733	CACATGAACACATTAAATGAGTCGAAGGTGTAGTAAAGAGTTCTCTTCTATTCATTTT	852
Db	541	CACATGAACACGTTTATACAGATCCAAAGGTGTAGTAAAGAGTTCTCTCGGAATATCATT	600
OY	853	ATTCAACATCGTTTGGAAAAGACTTACGTAGAAGCGGGGTTGTTGAACAGATATG	912
Db	601	ATTCATCATCGCTTGGAGAAAACCTACGTGGAAGGAAGACCTTCTGTGAACACACGAG	660
OY	913	ACTGTTATGTCGATATACATCTATACGAACACACATGAGATCTTACACGAATGGGTT	972
Db	661	ACGGCATTTGCACACACTACACCATTTGGAAAACCTCTGGCTCCCTTCATGAAATGGGTG	720
OY	973	TAAACA	978
Db	721	TAGAAA	726
RESULT 12			
LOCUS	AF383623	9258 bp	DNA
DEFINITION	Cloning vector PREXILC, complete sequence.		circular SYN 19-JUN-2001
ACCESSION	AF383623		
VERSION	AF383623.1	GI:14487946	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
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CDS			
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gene	/gene="bla"
	complement(8172. .9032)
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	DRMPRELNEAIPNDERDPTMPAAMATTLRKLLTGGELLTTSRQOLDDMEKDVAGPDL
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BASE COUNT	2108 a	2386 c	2604 g	2160 t
ORIGIN				


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Db      853  AAAAAAAAAAAAAAAAAAAAAA 873
RESULT 14
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LOCUS    AX250582      860 bp      DNA      linear      PAT 05-OCT-2001
DEFINITION Sequence 24 from Patent WO0168824.
ACCESSION AX250582
VERSION   AX250582.1  GI:15984331
KEYWORDS
SOURCE
ORGANISM Renilla reniformis.
           Renilla reniformis.
           Eukaryota; Metazoa; Cnidaria; Anthozoa; Aleyonaria; Pennatulacea;
           Sessiliflorae; Renillidae; Renilla.
REFERENCE
AUTHORS  1 (bases 1 to 860)
           Bryan, B.J., Szent-Gyorgyi, C. and Szczepaniak, W.
           Renilla reniformis fluorescent proteins, nucleic acids encoding the
           fluorescent proteins and the use thereof in diagnostics, high
           throughput screening and novelty items
           Patent: WO 0168824-A 24 20-SEP-2001;
           Prolume, Ltd. (US) ; Bryan, Bruce J. (US)
JOURNAL  Location/Qualifiers
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BASE COUNT  298 a      162 c      175 g      225 t
ORIGIN
Query Match      21.2%; Score 229; DB 6; Length 860;
Best Local Similarity 57.3%; Pred. No. 6; se-40;
Matches 454; Conservative 0; Mismatches 335; Indels 4; Gaps 2;
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Db      549  TTCAAACTTCACAACTGGCAACATTTCACTTACGACATGAGACAGCTTTACAAATCAAG 608
QY      820  GGTGTAGTAAAGAGACTTTCCTTGATGATCAATTTTATTCACATCGTTGGAAAGACTTAC 879
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QY      937  ATAGGAACCACTAGATCTCTTACACGATGGCTTTAAACACAGCTTACATTACTTTTC 996
Db      729  ATCAAAAAAATGAAAGGCTCTTAC-CATGATATCTATACACATTTATCTATAGCAGCT 787
QY      997  CAATTCGCTTTCATGCTCAATTAATTTTAAACATTTATGCAATGTTGTGATATG 1056
Db      788  ACCATTTTGGAAATATAGTGTATTGTTCAATAAATATTAATATAAAAAAAA 847
QY      1057  TTTGTAAAAAAA 1069
Db      848  AAAAAAAAAAAAAA 860
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RESULT 15
AF372525
LOCUS    AF372525      864 bp      mRNA      linear      INV 15-JUN-2001
DEFINITION Renilla reniformis green fluorescent protein (GFP) mRNA, complete
ACCESSION AF372525
VERSION   AF372525.1  GI:14161474
KEYWORDS
SOURCE
ORGANISM Renilla reniformis.
           Renilla reniformis.
           Eukaryota; Metazoa; Cnidaria; Anthozoa; Aleyonaria; Pennatulacea;
           Sessiliflorae; Renillidae; Renilla.
REFERENCE
AUTHORS  1 (bases 1 to 864)
           Szent-Gyorgyi, C.S. and Bryan, B.J.
           Luciferases, fluorescent proteins, nucleic acids encoding the
           luciferases and fluorescent proteins and the use thereof in
           diagnostics, high throughput screening and novelty items
           Patent: US 6232107-B 15-MAY-2001;
           Prolume Ltd.; 1085 William Pitt Way; Pitsburgh, PA;
           USA;
JOURNAL  Submitted (18-APR-2001) Prolume Ltd., 1085 William Pitt Way,
           Pitsburgh, PA 15238, USA
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BASE COUNT  295 a      164 c      178 g      227 t
ORIGIN
Query Match      21.1%; Score 227.4; DB 3; Length 864;
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Best Local Similarity 59.3%; Pred. No. 1,5e-39;
Matches 406; Conservative 0; Mismatches 276; Indels 3; Gaps 1;

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QY 280 AACACTTTGTTACAGAGTAATGCTATAAGTAATCTGGAAGTAATGTAAACAAC 339
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Db 193 AAGATATCGGTAAACAAAGCGCACACCTCCATCCGATTCGATTTGATATGCTGTGGCT 252
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QY 460 TTTCAATATGGCAACGCTTCTTACGAAATATCCGAATGATATATCAGATTATTTATA 519
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